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Sequence 2, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 7, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 41, Appl
Sequence 17, Appl
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Copyright (c) 1993 - 2004 Compugen Ltd.
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PCT-US95-03866-12
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444444400000004440000004440000000004440000	HESULT 1 1S-08-595-043A-50 Sequence 50, Application US/08595043A Patient No. 5935824 GENERAL INFORMATION: APPLICANT: SGARLATO, CREGORY D. TITLE OF INVENTION: PROTEIN EXPRESSI NUMBER OF SEQUENCES: 90 CORRESPONDENCE ADDRESS: ADDRESSEE: MEDLEN & CARROLL STREET: 220 MONTGOMERY STREET, SUI CITY: SAN FRANCISCO STATE: CALLFORNIA COUNTRY: UNITED STATES OF AMERICA ZIP: 94104 COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: BEALCATION DATA: MEDIUM TYPE: PLODS/MS-DOS SOFTWARE: PATENTIN: PC-DOS/MS-DOS SOFTWARE: PATENTIN: BC-DOS/MS-DOS SOFTWARE: PATENTIN: A35 APPLICATION NUMBER: 31-JAN-1996 CLASSIFICATION: A35 ATCRESTACATION: A35 ATCRESTACATION: PETER G. REGISTRATION NUMBER: 32, 837 REFERENCE/DOCKET NUMBER: 32, 837 TELEFONMUNICATION INFORMATION: TELEFONGE (415) 397-8338 INFORMATION FOR SEQ ID NO: 50: SEQUENCE CHARACTERISTICS: LENGTH: 232 amino acids TYPE: amino acid TYPE: ATCRESTY TYPE: protein SCOLOGY: linear MULECULE TYPE: protein	ப	KSCDKTHTCPPCPAPELLGGPS 	nayudgyeyhnyktkpreeqynstyrvusvlitylhonaangkeykckusnkalpapiekt
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00000000000000000000000000000000000000	A-50 Applicatic ORMATION: : SGARLATON: : SGARLATON: TENDEME ADDRE SEE: MEDILES SEE MEDILES SEAN FRANCIC CONTENT ON THE SEAN SEAN SEAN SEAN SEAN SEAN SEAN SEA	Similarity 5; Conserval	EPKSC 	TWYVE TWYVE
00000000000000000000000000000000000000	LT 1 8-95-043A-50 quence 50, Application tent No. 15955824 APPLICANT: SGALLATO, TITLE OF INVENTION: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS ADDRESSEE: MEDLEN & STREET: 220 MONTGO, CITY: SAN FRANCISC STARE: SAN FRANCISC STARE: SAN FRANCISC STARE: PALO4 COUNTRY: UNITED STR COMPUTER READABLE FORW MEDIUM TYPE: Floppy COMPUTER: 1BM FC CAROLL, PETI REFERENCE/DOCKET NUMBER: REFERENCE/DO	ch al si 225;	д д	61 1
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APPLICANT: Hackey, William F
APPLICANT: Hammang, Joseph F.
APPLICANT: Baetge, E. Edward
TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
Length 331;
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                                             Indels
  Score 1225; DB 3;
Pred. No. 5.6e-116;
3; Mismatches 4;
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CURRENT PEPLICATION NUMBER: uS/09/761,413
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US/09/178,869
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
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US-09-180-100-11
; Sequence 11, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 630639510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09761413
Patent No. 6506891
GENERAL INFORMATION:
APPLICANT: Tao, Weng
APPLICANT: Wong, Shou
97.2%;
                                             Conservative
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les 225; Conservative
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Query Match
Best Local Similarity
Matches 225; Conserv
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Patent No. 6797433

GENERAL INFORMATION:
BAPLICANT: Sun, Lee-Hwei K

APPLICANT: Sun, Bill

APPLICANT: Sun, Bill

APPLICANT: Sun, Cecily R

APPLICANT: Sun, Cecily R

APPLICANT: Sun, Cecily R

TITLE OF INVENTION: increased biological activities
FILE REFERENCE: 035UNNO01

CURRENT APPLICATION WUMBER: US/09/968,362A

CURRENT FILING DATE: 2001-10-01

NUMBER OF SEQ ID NOS: 28

SEQ THARE: PatentIn version 3.1

SEQ ID NO 26

LENGTH: 232
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Sequence 2, Application US/09178869B

Patent No. 6197294

GENERAL INFORMATION:

APPLICANT Tao, Weng

APPLICANT Hockey, William F

APPLICANT Hammang, Joseph P

APPLICANT Hammang, Joseph P

APPLICANT Bactege, E Leward

TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION

FILE REPERENCE: 17810-043

CURRENT APPLICATION NUMBER: US/09/178,869B

CURRENT FILING DATE: 1938-10-26

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LEMBTH: 331
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97.2%; Score 1225; DB 4;
Best Local Similarity 97.0%; Pred. No. 3.4e-116;
Matches 225; Conservative 3; Mismatches 4;
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CRGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 371
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                                                                                                                                                                                                                                                                                                                         Length 371;
                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                             Score 1225; DB 1;
Pred. No. 6.6e-116;
3; Mismatches 4;
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10S-08457-918-7
1 Sequence 7, Application US/08457918
1 Patent No. 6117655
1 GENERAL INFORMATION:
1 APPLICANT: Capon, Daniel J.
2 APPLICANT: Gregory, Timothy J.
2 TITLE OFF INVENTION:
2 NUMBER OF SEQUENCES: 25
2 CORRESPONDENCE:ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 460 Point San Bruno Blvd CITY: South San Francisco STATE: California CONTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBALE FORM:
MEDIUM TYPE: 5.25 inch, 360 KD flg
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-LOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-UNM-1995
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MBER: US/08/457,918
1-JUN-1995
                                                                 144P1C2
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FILING DATE: 02 MAY-155-
PRIOR APPLICATION DATE: 07/936190
APPLICATION POWBER: 07/936190
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APPLICATION NUMBER: 08/236311
FILING DATE: 02/MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MBER: 07/842777
18-FEB-1992
                                   RACISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 444P1
TELECOMMUNICATION INFORMATION:
TELEFAX: 415/952-9881
TELEFAX: 910/317-7168
INFORMATION FOR SEQ ID NG: 7:
SEQUENCE CHARACTERISTIES:
                                                                                                                                                                                                                                                                                                                             97.2%;
ilarity 97.0%;
Conservative
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
                     NAME: Hasak, Janet E. REGISTRATION NUMBER:
                                                                                                                                                                                                                    LENGTH: 371 amino adi
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 225; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ISKAKYØPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NWYVDGVEVHNVÆTKPREFQYNSTYRVVSVLTVLHONWMGKEYKCKVSNKALPAPIEKT
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0
                                                                                                                                                                                                                                                                                                                                    Length 360;
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APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT APPLICATION NUMBER: PCT/JP97/01502
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER APPLICATION NUMBER: PCT/JP97/01502
SARIJER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SEQ TWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTRY: CALILORINIA
COMPUTRY: CALILORINIA
COMPUTRY: CALILORINIA
COMPUTRY: READABLE FORM:
MEDLUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTRY: IBM PC compatible
OPERATING SYSTEM: PC-DSS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,311
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
FILING DATE: 02-OCT-1987
                                                                                                                                                                                                                                                                                                                                    5; DB 3;
6.3e-116;
                                                                                                                                                                                                                                                                                                                                                       ed No. 6.3e.
Mismatches
                                                                                                                                                                                                                                                                                                                             Query Match
97.2%; Score 1225;
Best Local Similarity 97.0%; Pred No. 6...
Matches 225; Conservative 3; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 71, Application US/08236311
Patent No. 556335
GENERAL INFORMATION:
APPLICANT: Capper, Daniel J.
APPLICANT: Gregory, Timothy J.
TILLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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07/250785

APPLICATION DATA:

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319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             320 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 371
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US-09-180-100-22

Sequence 22, Application US/09180100

Patent No. 6306395

GENERAL INFORMATION:
APPLICANT: NAKAMURA, No. 6306395io

APPLICANT: NAKAMURA, No. 6306395io

TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
PILE REFERENCE: 1110-207P

CURRENT APPLICATION NUMBER: US/09/180,100

CURRENT FILING DATE: 1998-11-02

BARLIER PILING DATE: 1998-11-02

BARLIER FILING DATE: 1998-11-02

BARLIER FILING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PATENTING VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

97.2%; Score 1225; DB 4;
Best Local Similarity 97.0%; Pred. No. 6.6e-116;
Matches 225; Conservative 3; Mismatches 4;
                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444PIC3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                        FILING DATE: 28-SEP-1988
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
                                                                                                                                                                                                                                                  TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ 1D NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                  TELEPHONE: 415/225-8228
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Matches 225; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-180-100-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ISKAKVOPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
COMPUTER IEADABLE FORM:
COMPUTER: 1EM PC compatible
CURRENT APPLICATION DATA:
RILING DATE: 28-May-2002
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.2%; Score 1225; DB 3;
97.0%; Pred. No. 6.6e-116;
live 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/10157408
Fatent No. 6710169
GENERAL INFORMATION:
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OR APPLICATION DATA:
APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-UUN-1995
APPLICATION NUMBER: 08/236311
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 07/936190
APPLICATION NUMBER: 07/842777
                                                                                            NAME: KUDINGC, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERNCE/OCKET NUMBER: P0444PLC3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-828
TELEFAX: 415/522-9881
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 18-FEB-1992
                        07/104329
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/10
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
                                                                                                                                                                                                                                                                                                                                    371 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 97.0
Matches 225, Conservative
                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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APPLICANT: BARTHIK, Eckart
APPLICANT: BIDENVUELLER, Bernd
APPLICANT: BIDENVUELLER, Bernd
APPLICANT: BIDENVUELLER, Bernd
APPLICANT: BUETINER, Prank
APPLICANT: HUGHES, Clare
APPLICANT: HUGHES, Clare
APPLICANT: HUGHES, Clare
APPLICANT: HUGHES, Clare
APPLICANT: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: Aggrecanase" in cell culture systems
TITLE OF INVENTION: Aggrecanase" in cell culture systems
ADDRESSEE: Foley & Lardner
STREET: Suite S00, 3000 K street, N.W.
COUNTRY: Usa shington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 BPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                             181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVWHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                               345 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVWHEALHNHYTQKSLSLSPGK 396
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ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/176,228
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Best Local Similarity 97.0%; Pred. No. 7.3e-116;
Matches 225; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
FRICK APPLICATION DATA:
APPLICATION NUMBER: US/08/784,512
FILING DATE: 17-7AN-1997
APPLICATION NUMBER: EF 96100682.2
FILING DATE: 18-7AN-1996
ATOCNEY AGENT INFORMATION:
NAME: GRANADOS, PATRICIA D.
REGISTRATION NUMBER: 33,683
REGISTRATION NUMBER: 33,683
REGISTRATION NUMBER: 18748/311
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09176228 Patent No. 6180334 GENERAL INFORMATION:
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein
LOCATION: 1..396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-176-228-3
                                                                                                                                                                                                                                                                                                   RESULT 11
US-09-176-228-3
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Sequence 3, Application US/08784512
Patent No. 5872209
GENERAL INFORMATION:
APPLICANT: BATTNIK, Eckart
APPLICANT: EIDENWUELLER, Bernd
APPLICANT: BUSTTNER, Frank
APPLICANT: HUGHES, Clare
APPLICANT: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
CORRESPONDENCE: ACCORDENCE: ACCORDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ISKAKVQPREBÇUYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
265 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRIPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                  325 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 376
                                                                                                                                                                             181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 & Street, N.W.
CITY: Washington, D.C.
COUNTR: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYRE: Flappy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,512
FILING DATE: 17-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 9610682.2
FILING DATE: 18-JAN-1966
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, PATICIA D.
REFERENCE/DOCKET NUMBER: 18748/311
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202, c. TELEFAX: (202, c. TELEFAX: 904136
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 396 amino acids TVPE: amino acid mype: "TVPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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LOCATION: 1.396
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                PCT-US95-03866-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US95-03866-14
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285 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180
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                                                                                                                                         345 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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                                                                                                 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1225; DB 5; Length 4
Pred. No. 8e-116;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                               Sequence 12, Application PC/TUS9503866

Sequence 12, Application PC/TUS9503866

GENERAL INFORMATION:
APPLICANT: Cobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DINRR OF KIT LIGAND TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
CORRESPONDENCES: 36
CORRESPONDENCE: 36
ADDRESSEE: Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUDRESSEE: Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY: United States of America COUNTRY: United States of America COMPITED: New York COUNTRY: United States of American COMPITED: New York COUNTRY: United States of American COMPITED: No. 200 Perican Compited COMPITED: No. 200 Perican CompiteD CompiteD
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
AFFLING DATE: 28-WAR-1994
ATTORNEY, AGENT INFORMATION:
NAME: Haley dr, James F
REGISTAATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: CytoMed/2
TELECHONE: 212-556-9090
TELECHAN: 212-556-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CytoMed/2
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amino acid
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Best Local Similarity
Matches 225; Conserv
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193 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ISKAKVOPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPBVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·,
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PCT-US96-10043-11
Sequence 11, Application PC/TUS9610043
GENERAL INFORMATION:
HAPPLICANT: The General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.2%; Score 1225; DB 5; Length 424; 97.0%; Pred. No. 8e-116; Live 3; Mismatches 4; Indels
                                               APPLICANT: CytoMed, Inc. (all states except US)
APPLICANT: CytoMed, Rarl (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
TITLE OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,379
FILING DATE: 28-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr. James F
REGISTRATION NUMBER: 27,794
REFENCE/DOCKET NUMBER: CytoMed/2
TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                                                    STATE: New York COUNTRY: United States of America ZIP: 10020
Sequence 14, Application PC/TUS9503866 GENERAL INFORMATION:
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amino acid
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Best Local Similarity 97.0°
Matches 225; Conservative
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MOLECULE TYPE: protein
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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Pred. No. 8.4e-116;
3; Mismatches 4; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Security 25 88A-7 Security 25 88A Security 26 88A-72-88BA-7 Sequence 7, Application US/0847288BA Sequence 7, Application US/0847288BA Sequence 7, Application US/084728BBA Security 6613746 GENERAL INFORMATION: Brian APPLICANT: Welz, Gerd APPLICANT: Welz, Gerd TITLE OF INVENTION: AND RELATED MOLECULES AND METHODS NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS: ADDRESSE: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-BOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION UNDERER: US 60/000,213
FILING DATE: 14-UN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER:
                                                                                                                                                   Fish & Richardson P.C
TITLE OF INVENTION: AND METHODS NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 437 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 97.0%;
Matches 225; Conservative
                                                                                                                                                                                                                                                                                       STATE: MA
COUNTRY: USA
ZIP: 02210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PC compa
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CLASSIFICATION:
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3: Clark & Elbing LLP 176 Federal Street

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271 NWYVDGVEVHNAKTKPREEQXNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         331 İSKAKGÓPREPQVYTLPPSKDELTKNQVSLTCLVKGPYPSDIAVEWESNGÓPENNYKTTP 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1225; DB 4; Length 442;
Pred. No. 8.5e-116;
3; Mismatches 4; Indels
COMPUTER READBLE FORM:
MEDIUM TYDE: Diskette
COMPUTER: IBM Compatible
OOPEVATURG SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,888A
FILING DATE: 07-UWN-1995
CLASSIFICATION A 424
PRIOR APPLICATION DATE: 07/618,314
PRIOR APPLICATION NUMBER: 07/618,314
PILING DATE: 22-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAMME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 00786/258001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: October 27, 2004, 17:05:53 Job time : 24:1174 secs
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Best Local Similarity 97.0%;
Matches 225; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 442 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617-428-7045
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MOLECULE TYPE: protein
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Ig gamma-1 chain C
Ig gamma-3 chain C
Ig gamma-2 chain C
Ig gamma-2 chain C
Ig gamma-2 chain C
Ig gamma-1 chain C
Ig gamma 2b chain
Ig gamma 2b chain
Ig gamma 2b chain
Ig gamma 1 chain C
Ig gamma 1 chain C
Ig gamma-1 chain C
Ig gamma-2 chain C
Ig gamma-2 chain C
Ig gamma-1 chain C
Ig gamma-2 chain C
Ig gamma-1 chain C
Ig gamma-3 chain
Ig gamma-3 chain
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Ig gamma-2 chain
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Ig gamma-2 chain
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                                                                                                                                                                                                                                                                                             1 ASTKGPSVFPLAPSSKSTSG......MHEALHNHYQQRSLSLSPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      otal number of hits satisfying chosen parameters:
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Maximum Match 100%
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3: pir3:*
4: pir4:*
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Match
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erfect score:
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•	Ig gamma-2c chain	Ig gamma-2a chain	Ig gamma-2a chain			Ig gamma-2b chain	Ig gamma-2b chain	gamma 4 cha		Ig epsilon chain C	Ig heavy chain VHI	heavy chain	Ig heavy chain pre	gamma-1 chai	Ig gamma-1 heavy c	Ig heavy chain (DO
	S00847	S40295	PS0019	806611	GZMSBM	S01321	G2MS11	147162	146732	S38864	S69340	A36040	S04845	S14236	A49444	869131
											7					
	329	446	322	327	405	475	474	277	180	548	249	218	549	152	220	241
	61.5	61.1	60.9	60.3	59.8	58.9	58.8	58.3	37.9	36.8	31.1	31.0	31.0	30.7	30.3	30.2
	1085.5	1078	1074	1063.5	1054	1039	1036.5	1028	699	648.5	549	547	547	542	534	532
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Cypecies: Homo sapiens (man)
Cypecies: Homo sapiens (man)
Cypecies: Homo sapiens (man)
Cypeces: 20-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
Cypeces: 20-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
Rythuck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Rythuck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Rythuck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
AyTille: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: CA; Residues: 1-377 chuc.
A; Reference number: A23511; MUID:86148507; PMID:3081877
A; Residues: 1-377 chuc.
A; Residues: 1-377 chuc.
A; Residues: 1-377 chuc.
A; Residues: 1-377 chuc.
A; Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C; Genetics: GB:I19339; OMIM:147120
A; Map position: 14G2.33-14G32.33
A; Cross-references: GB:I19339; OMIM:147120
A; Map position: 14G2.33-14G32.33
A; Cross-references: B4/3, 115/3; 115/3; 116/3; 120/3; 270/3
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Reywords: immunoglobulin homology ciMM>
F; 20-85/Domain: immunoglobulin homology ciMM>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 280-2857, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, C3, C5, u) with an IGHG4
A;Reference number: A60764; MuID: 90007613; PMID: 2571587
A;Accession: A60764
A;Accession: A60764
A;Residues: Dreliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPROT: Q8N4Y9
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV-
                                                                                chain C region (allotype G3m(b))
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igen Primaerstruktur.

A; Reference numbers: A91668; MUID:77070269; PMID:826475

A; Contents: myeloma protein Nie

A; Accession: B9168

A; Anclecule type: protein

A; Redicule type: protein

A; Residues: 1-34, '0', 36-96, 'K', 98-115, '0', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27

A; Note: this sequence has the GIm(17) and GIm(1) markers

R; A; Schmidd', W.E.; Jung, H.D.; Palm, 'W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 364, '711-193 A7, 1963

A; Title: Die Primaerstruktur des Kristallisierbaren monoklonalen Immunglobulins IgG1 KOL

A; Reference number: A91723; MUID:81289131; PMID:6884994

A; Reference number: A91723

A; Reference number: A91723

A; Reference number: A91723

A; Residues: 1-96, 'R', '88-197, 'D', '199-238, 'E', '240, 'M', '242-266, 'D', 268-271, 'D', '273-330 cSCH

A; Residues: 1-96, 'R', '88-197, 'D', '199-238, 'E', '240, 'M', '242-266, 'D', 268-271, 'D', '273-330 cSCH

A; Residues: 1-96, 'R', '88-197, 'D', '199-238, 'E', '240, 'M', '242-266, 'D', 268-271, 'D', '273-330 cSCH

A; Residues: 1-96, 'R', '88-197, 'D', '199-238, 'E', '240, 'M', '242-266, 'D', 268-271, 'D', '273-330 cSCH

A; Residues: 1-96, 'R', '88-197, 'D', '199-238, 'E', '240, 'M', '242-266, 'D', 268-271, 'D', '273-330 cSCH

A; Residues: 1-96, 'R', '88-197, 'D', '199-238, 'E', '240, 'M', '242-266, 'D', 268-271, 'D', '273-330 cSCH

A; Reference number: A90565; MIDID:1106427; PMID:11002129

A; Contents: annotation; disulfide bonds
A; Reference number: A10667; MIDID:1002129
A; Reference number: A10667; MIDID:1002129
A; Reference number: A10667; MIDID:1002129
A; Reference number: A10667; PMID:1002129
A; Reference number: A10667; PMID:1002129
A; Reference number: A10667; PMID:1002129
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A;Cross-references: GDB:120085; OMIM:147100
A;Map pooition: 14622.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C;Complex: An immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology cimto C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology cimto F;137-266/Domain: immunoglobulin homology cimto F;137-266/Domain: immunoglobulin homology cimto F;137-83;144-204, 250-386/Disulfide bonds: #status experimental F;109,112/Disulfide bonds: interchain (to light chain) #status experimental F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental
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Pred. No. 2.4e-112;
3; Mismatches 4;
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A,Gene: GDB:IGHG1
A,Cross-references: GDB:120085; OMIM:147100
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Best Local Similarity 97.9%;
Matches 323; Conservative
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Query Match Local 61

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194

301 314 361

254

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A,Map position: 1462-33-1462-33
A)Map position: 1462-33-1462-33
C;Complex: An immunoglobulin heteroterramer subunit consists of two identical light (kapp hain disulfide bonds: In some cases, such as IgA and IgW, the subunits associate into lan c;Complex: An immunoglobulin c region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin C;Reywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology < IML>
F;20-85,Domain: immunoglobulin homology < IML>
F;33-306/Pomain: immunoglobulin homology < IM3>
F;34-102,Domain: immunoglobulin homology < IM3>
F;14-102,103,106,109/Disulfide bonds: interchain (to light chain) #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;105/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                   residues 25, 59, 60, and 264-268
that shown in having 60-Ala and in the amidatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 LIKNQVSLITCLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSVGSFFLYSKLTVDKSRW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig gamma-4 chain C region - human C;Species Homosapiens (man) (2,Species: Homosapiens (man) (man) C;Species: Homosapiens (man) C;Date: 02-Apr-1962 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004 C;Accession: A90933; A90249; A02150 Ms. I. Buxbaum, J.; Hood, L. DNA 1, 11-18, 1981 homosapiens of a human immunoglobulin C-gamma4 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 STFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                human immunoglobulin G2
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                                                                                                                                                                                                                                                                                                 RiMilstein, C.; Frangione, B.
Bochem. O. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immu A;Title: Disulphide bridges of the heavy chain of human immu A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Reference number: A90253; MUID:72033500; PMID:4940472
R;Frangione, B.; Milstein, myeloma protein Sa, disulfide bonds R;Frangione, B.; Milstein, C.; Pink, J.R.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Structural studies of immunoglobulin G. A; Reference number: A93157; MUID:69064124; PMID:5782707 A; Contents: annotation; Sa, disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.8%; Score 1566; DB 1;
89.1%; Pred. No. 4.4e-101;
tive 15; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 OCGNVFSCSVMHEALHNHYOORSLSLSPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GDB:119338; OMIM:147110
A, Accession: A93132
A, Molecule type: protein
A, Residues: 238-275 - 406.
R, Hoffmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A, Reference number: A94591
A, Contents: annotation; Zie, revisions to
A, Note: the revised sequence differs from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 89.1%
Matches 294; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: GDB:IGHG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
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'Species: Home saptens (man)
'Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
'Accession: A93906; A92809; A90752; A93132; A02148
'Accession: A93906; A92809; A97809; A93132; A02148
'Ellison, J.; Hood, L.
roc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
'Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con 'Accession: A93906; MUID:82197621; PMID:6804948
'Accession: A93906
'Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: protein
Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-
Note: this sequence has since been revised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hofmann, T.; Farr, D.M.
ol. Immunol. 16, 923-925, 1979
iffile: A note on the amino acid sequence of residues 381-391 of human immunoglobulin Faference number: A93132; MUID:80114419; PMID:118920
;Contents: Zie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Residues: 1.326 cELL>
;Gross_references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1;
;Note: Lys-326 is probably removed posttranslationally
;Note: Lys-326 is probably removed posttranslationally
;Namny, A.C.; Tung, E.; Fudenberg, H.H.
Immunol. 125, 1048-1054, 1980
;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and
;Reference number: A92809; MUID:81007873; PMID:6774012
;Accession: A92809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title: The amino acid sequences of the three heavy chain constant region domains of Reference number: A90752; MUID:80001357; PMID:113060 Contents: myeloma protein Zie
                                                                                                                                                                                                                                                                                                                                                                              GLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 ODWINGKEYKCKVSNKALPAPIEKTISKTKGÓPREPQVYTLPPSREEMTKNQVSLTCLVK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLH 193
                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                 1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 DIPPPCPRCPEPKSCDIPPPCPRCPEPKSCDIPPPCPRCPADELLGGPSVFLFPPKFKDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 IMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GFYPSDIAVEWESNGOPENNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT
                                                                                                                                                                                                          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                               Gaps
                                                                                                                                           47;
                                                                            Length 377;
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| Residues: 1-19, (0', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 < WAN>

| Note: Trp-156 is at or near the complement-binding site

| Connell, G.E., Barr, D.M.: Hofmann, T.

an. J. Biochem. 57, 758-767, 1979
                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                           GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV-----
                                                                            DB 2;
                                                                                                               1.1e-102;
                                                                         90.2%; Score 1590.5;
80.1%; Pred. No. 1.1e
                                                                                                                                           13; Mismatches
          20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALHNHYQQRSLSLSPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALHNRFTQKSLSLSPGK 377
                                                                                                                                        Matches 302; Conservative
                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 TATYYCGYSVEGYGQGYRFHSWGQGTLVTVSSEPKSCDKTHTCPPCPAPELLGGPSVFLF 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 PSVFIFPPXPXDTLMISRTPOVTCVVVDVSOENPEVOPSWYVDGVEVHTAQTRPKEEQFN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLYSLSSVVTVPSSSLGTQTYICNVHKPSNTKVDKKVFPKSCDKTHTCPPCPAPELLGG 120
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Species: Sus scrofa domestica (domestic pig)
Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVLTVLHQNMMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLICLVKGFYPSDIAVEWESNGOPENNYKTIPPVLDSVGSFFLYSKLIVDKSRWQQGNVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 TQTYICNVN-----HK-PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNSTYRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
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                                                                               A; Cross-references: EMBL:X81695
B; Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A; Reference number: S72664
A; Accession: S72664
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-140, C', 142-374 «KH2>
A; Ross-references: EMBL:X81695
C; Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.5%; Score 1225.5; DB 2; 87.1%; Pred. No. 1.8e-77; tive 6; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 69.4%; Score 1225; DB 2; al Similarity 67.5%; Pred. No. 1.7e-77; 224; Conservative 46; Mismatches 56:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 87.1%;
Matches 230; Conservative
                                                      A;Residues: 1-374 <KHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127
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A; Accession: A90933; MUID:83157104; PMID:6299662
A; Accession: A90933
A; Molecule type: DNA
A; Mesidues: 1-32 v Edib.
A; Cross-references: UNIPROT: P01861
A; Note: the sequence was determined from the germline gene
R; Pink, V. attery: S.H.; De Vries, G.M.; Milstein, C.
B; Biochem. J. 117, 33-47, 1970
A; Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant of the first form the protein or number: A90249; MUID: 70207560; PMID: 4192699
A; Molecule type: protein
A; Molecule type
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Crispecies: Homo sapiens (man)
Crispecies: Homo sapiens (man)
Crispecies: Homo sapiens (man)
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Crispecies: Homo sapiens (man)
Crispecies: Homo sapiens (man)
Crispecies: State sapiens (man)
Crispecies: A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Rithe: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A; Reference number: S69339; MulD:95262687; PMID:7744049
A; Accession: S69339
A; Accession: S69339
A; MulD:95262687; PMID:7744049
A; Mulcheule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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F:240-307/Domain: immunoglobulin homology <IM3>
F:240-307/Domain: immunoglobulin homology <IM3>
F:241/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:107/Binding site: carbohydrate (Asn) (covalent) #status predicted
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larity 88.8%; Pred. No. 3.8e-100;
Conservative 15; Mismatches 19;
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Best Local Similarity
Matches 293; Conserv
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                                              2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLYSLSSVYTVPSSSLGTQTYTCHVVNHKPSNTKVDFKSCDXTHTCPPCPAPELLGG 120
                                                                                                                                                                                                           61 GLYSLSSMYTVPASSLSSKSYTCNVNHPATITTKVDKRVGTKTKPPCPICPACESP---G 116
                                                                                                                                                                                                                                                                           PSVFLPPPKPXDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
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C,Species, Sus screfa domestica (domestic pig)
C,Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C,Accession: 147158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 SNIKVDKKVEPKSCDKIHICPPCPAPELLGGPSVFLFPPKPKDTLMISRIPEVICVVVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 SHEDPEVKENWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 ALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
                                                                                                                   1 APKTAPLVYPLAPCGRDTSGPNVALGCLASSYFPEPVTVTWNSGALTSGVHTFPSVLQPS
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                                                                                        1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                 9
    Length 328;
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A,Residues: 1-234 <EER>
C,Superfamily: immunoglobulin C region; immunoglobulin homology
C,Keywords: immunoglobulin
F,48-117/Domain: immunoglobulin homology <IMM>
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                                              Indels
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R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-327, 1991
A;Title: Nucleotide sequence of chimpanzee Fc and hinge
A;Reference number: PT0207; MUID:91287716; PMID:2062315
A;Accession: PT0207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.9%; Score 1216; DB 2;
95.7%; Pred. No. 4.6e-77;
tive 4; Mismatches 6;
                                                 58;
ttch 69.1%; Score 1219; DB 2; cal Similarity 67.2%; Pred. No. 4.3e-77; 223; Conservative 45; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 SWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 RWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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Best Local Similarity 95.73
Matches 224; Conservative
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       Query Match
Best Local S:
Matches 223
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PT0207
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                                                                                                                                                                                                                                                                                                                                                                         Note: Homo sapiens (man) gene engineered and expressed in Escherichia colibate. Homo sapiens (G-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000 Accession: 831866
Filpula, D. bmitted to the EMBL Data Library, February 1993
Description: Screeing method for protein-protein interactions of cloned gene products. Reference number: 831866
Accession: 831866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ๗
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Immunol. 153, 3565-3573, 1994
intile: Five putative subclasses of swine IgG identified from the cDNA sequences; Reference number: 147158; MUD:95015845; PMID:7930579
;Accession: 147160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAPIEKTISKAKVOPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPE 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDPEVKENWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKAL 211
                                                                                                                               NNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNYQQRSLSLSPGK 330
            STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 TVAQADVESKSCDKTHTCPPCFAPELLGGPSVFLFPFRKDTLMISRTPEVTCVVVDVSH 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  j gamma 2b chain constant region - pig (fragment)
Species: Sus scrofa domestica (domestic pig)
Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                    Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
                                                                                                       241 LIKNOVSLICLVKGFYPSDIAVEWESNGO--PENNYKTIPPVLDSVGSFFLYSKLIVDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: mRNA
Residues: 1-255 <FIL>
Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keywords: immunoglobulin
1-22/Region: Escherichia coli outer membrane protein A precursor
23-255/Region: human Ig gamma-1 chain C region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 94.6%; Pred. No. 2e-77; 26; Conservative 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene: IgG2b
Superfamily: immunoglobulin C region; immunoglobulin homology;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; translated from GB/EMBL/DDBJ.
Wolecule type: mRNA
:Residues: 1-328 <KAC>
                                                                                                                                                                                                                        297 SWOGGGIFQCAVMHEALHNHYTQKSISKTPGK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - pig (fragment)
                                                                                                                                                                                               299 RWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
                                                                                                                                                                                                                                                                                                                                                               gamma-1 chain C region - synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: 147160
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Matches 226;
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152 77 212

Query Match

272 197

Genetics:

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Query Match
Best Local Similarity 67.9
Matches 222; Conservative
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   A.Tatle. Tive putative subclasses of swine IgG identified from the cDNA sequences of A.Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A.Feference number: 147158; MUD:95015845; PMID:7930579
A.Accession: 147158
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: 1-328 cKAC>
A.Cross-references: EMBL:U03778; NID:9433121; PIDN:AAA52216.1; PID:9433122
A.Genetics:
A.Genetics:
A.Genetics:
C.Superfamily: immunoglobulin C region; immunoglobulin homology
F/133-202/Domain: immunoglobulin homology cIMM>
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                                                                                                                                                                                                                                                                  GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
                                                                                                                                                                                                                                                                              61 GLYSLSSMVTVPASSLSSKSYTCNVNHPATTTKVDKRV---GIHQPQTCPICPGCE-VAG 116
                                                                                                                                                                                                                                                                                                                121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPBVKFNWYVDGVEVHNVKTKPREEQYN 180
                                                                                                                                                                                                                                                                                                                             236
                                                                                                                                                                                                                                                                                                                                                                                                                            241 LIKNQVSLICLVKGFYPSDIAVEWESNGQ--PENNYKTIPPVLDSVGSFFLYSKLIVDKS 298
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                                                                                                                                                                                                                  1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                             181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
                                                                                                                                                                                             Gaps
                                                                                                                                                                                             9
                                                                                                                                                                      Length 328;
                                                                                                                                                                                            61; Indels
                                                                                                                                                                  cch 67.6%; Score 1193; DB 2; al Similarity 67.2%; Pred. No. 2.7e-75; 223; Conservative 42; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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I.; Sun, J.;
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                                                                                                                                                                   Match
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Matches
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A;Note: this sequence has the dil allotypic marker, 104-Met, and the els allotypic mark R;Fruchter, R.G., Jackson, S.A.; Mole, L.E.; Porter, R.R.
Bjochem. J. 116, 249-259, 1970
A;Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin A;Reference number: A90245; MUD:70110015; PMID:5461106
A;Accession: A90245
A;Molecule type: protein
A;Residues: 132-143, E',145-161
A;Residues: 132-143, E',145-161
C;Rill: R.L.; Lebovitz. H.E.; Fellows Jr., R.E.; Delaney, R.
In Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell A;Reference number: A94416
A;Reference number: A94416
A;Residues: 129-131;155-172, 'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q'
A;Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q'
A;Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q'
A;Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q'
A;Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q'
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kaj hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into li C;Superfamily: immunoglobulin heterotetramer; immunoglobulin creation; electrotetramer; immunoglobulin homology cint.
F;20-62/Domain: immunoglobulin homology cint.
F;20-62/Domain: immunoglobulin homology cint.
F;216-303/Domain: immunoglobulin homology cint.
F;216-303/Domain: immunoglobulin homology cint.
F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gramma 3 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147161
R;Kacskovics, I:; Sun, J.; Butler, J.E.
J. Immunol. 153, 356-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a sAccession: 147161
A;Reference number: 147188; MUD:95015845; PMID:7930579
A;Accession: 147161
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-328 «KAC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVVSVLTVLHQNMMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTK 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: IgG3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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A,Reference number: A90354; MUID:71058474; PMID:4922544
A,Contents: annocation; disulfide bonds
A,Note: Cys-16; is involved in a heavy-light chain bond
A,Note: Cys-16; Cys-107, and Cys-110 form inter-heavy chain bonds
A,Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C,Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp c,Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp c,Complex: An immunoglobulin heterotetramer; immunoglobulin heavy c,Reywords: duplication; glycoprotein; immunoglobulin homology
C,Reywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;138-204/Domain: immunoglobulin homology <IM3>
F;241-310/Domain: immunoglobulin homology <IM3>
F;28-79/Disulfide bonds: #status experimental
F;142-202/Disulfide bonds: #status experimental
F;178/Binding site: carbobydrate (Asn) (covalent)
F;248-308/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DELIKNQVSLICLVKGFYPSDIAVEWESNGQP--ENNYKTIPPVLDSVGSFFLYSKLIVD 296
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession: S31459
R;Patri, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
A;Reference number: S31459
A;Accession: S31459
A;Acteus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ARTTAPSVFPLAASCVDISGSMMTLGCLVKGYFPEPVTVKWNSGALISGVHTFPAVLQ-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GLYSLTSMYTVPSSQKAT----CNVAHPASSTKVDKTVEPIRTPZPBPCTCPKCPPPENL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 GGESVEIFPPKRKDTLMISLTPRVTCVVVDVSQDEPEVQFTWFVDNKPVGNAETKPRVEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 YNTTERVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPRYPDVYTLPPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH--TCPPCPAPELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 GGPSVFLFPPKPKDTLMISRIPEVICVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQ
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; Pred. No. 4.7e-73;
40; Mismatches 71; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 329;
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A;Residues: 1-472 <PAT>
A;Cross-references: EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;277-346/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

66.6%; Score 1174.5; DB

Best Local Similarity 68.2%; Pred. No. 5.2e-74;

Matches 227; Conservative 31; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297 KSAWDQGTVYTCSVWHEALHNHVTQKAISRSPG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 KSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPG 329
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Best Local Similarity 65.7%;
Matches 218; Conservative 4
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Lochemistry 13, 4796-4803, 1974
Cochemistry 13, 4796-480 of the C-H2 homology region from guinea pig IgG2 antibodies.
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Residues: 13 < rm. 13 cm.
Cross-references: UNIPROT:P01862
Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
.ochemistry 10, 18-25, 1971.
Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III.
Reference number: A90352; MUID:71058471; PMID:5538606
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Residues: 227-311 -TR2>
.Oliveira, B.; Lamm, M.E.
iochemistry 10, 26-31, 1971
.Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
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Species: Cavia porcellus (guinea pig)
Date: 07-May-1981 #sequence revision 07-May-1981 #text change 09-Jul-2004
Accession: A94553; A90352; A90389; A90384; A90385; A02<u>1</u>51
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                   ; Score 1189; DB 2;
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43; Mismatches 61;
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Danited to the Atlas, April 1975
Reference number: A94553
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Residues: 134-226 <TRA>
Trischmann, T.M.; CBDra, J.J.
ochemistry 13, 4804-4811, 1974
Title: Primary structure of the
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October 27, 2004, 16:32:53 ; Search time 149.733 Seconds (without alignments) 1268.081 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. 1 protein - protein search, using sw model in on:

US-10-000-439-2 1764 1 ASTKGPSVFPLAPSSKSTSG.......MHEALHNHYQQRSLSLSPGK 330 tle: rfect score:

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36	Eukaryota; Metazoa; Mammalia: Entheria:	Metazoa; Chordata; Antheria: Primates:	Catarrhini: Hominidae;	, 10000
2 8	NCBI TaxID=9606;			
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RP	SEQUENCE FRO	M N.A.		
×	MEDLINE=8227	4238; PubMed=62	MEDLINE=82274238; PubMed=6287432;	
5 E	Ellison J.W.	, Berson B.U.,	HOOG L.E.;	. andp
7 L	Nine increor	"ine nucleotide sequence of a numan f	,	, , ,
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RX.	MEDLINE=71064024;	4024; PubMed=5489771;	89771;	
R.	Cunningham B	.A., Rutishause	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,	
æ	Waxdal M.J.,	Edelman G.M.;		
E I	"The covalen	it structure of	a human gamma G-ımmunoglobulın.	Vii. Amino
E i	acid sequence	e of heavy-chai	of heavy-chain cyanogen bromide Iragments HI-H4."	
7 2	Blochemistry	A:310/15-T9T5:6	. (0)	
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4 X	MEDLINE=7106	MEDLINE=71064025: PubMed=5530842;	30842;	
RA.	Rutishauser	U., Cunningham	B.A., Bennett C., Konigsberg W.H.,	'n
Æ	Edelman G.M.;	,		
RT	"The covalen	it structure of	covalent structure of a human gamma G-immunoglobulin. 8.	8. Amino
RT	acid sequenc	e of heavy-chai	n cyanogen bromide fragments H5-	-H7.";
RL	ซ	9:3171-3181(19	.40).	
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КP	SEQUENCE (MY	SEQUENCE (MYELOMA PROTEIN NIE)	IIE).	
RX	MEDLINE=7707	MEDLINE=77070269; PubMed=826475;	:6475;	
Ą	Ponstingl H.	, Hilschmann N.		•
RI	"The rule of	antibody struc	ure. The primary structure of	a monocional
RT	IgG1 immunog	lobulin (myelom	a protein Nie). III. The Chymoti	ryptic
RT	peptides of	the H-chain, al	ignment of the tryptic peptides	ana
RT	discussion c	of the complete	structure.";	
H.	Hoppe-Seyler's Z.	's Z. Physiol.	Physiol. Chem. 357:1571-1604(1976).	
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RP	SEQUENCE (MY	ELOMA PROTEIN R	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.	
X :	MEDLINE=8328	39131; PubMed=68	184994;	
¥ !	SCHMICE W.E.	, .uH gran,	ALIM W., HILBCIMIAIN N.;	,
	"Three-dimer	sional structur	e decermination of antibodies.	FILMALY
KT.	structure of	crystallized m	structure of crystallized monoclonal luminogroupin 1961 NO	
	Hoppe-Seyle1	's Z. Physiol.	Chem. 364:713-747(1983).	
2 E	[6]	(b)		

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N-linked (GlcNAC. ..).
K -> R (in Glm(3) marker).
FTId=VAR 003886.
D -> E (in Glm(non-1) marker).
FTId=VAR 003887.
L -> M (in Glm(non-1) marker).
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T and its complex with fragment and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus arreus at 2.9- and 2.8-A resolution.";

Elechemistry 20:2361-2370(1981)

MESCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the GIM(3) markers and the GIM(17) allotypic marker, 97-K, and the GIM(3) markers and the GIM (10n-1) markers.

HIS, 198, 269 and 272.

MESCELLANEOUS: BU also differs in the amidation states of 35, 116, 198, 269 and 272 and in the order of residues 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
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                                                                 DISULFIDE BONDS.
MEDLINE=77070267; PubMed=1002129;
MEDLINE=77070267; PubMed=1002129;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Nule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (upeloma protein Nie), I: purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                            -!- MISCELLANEOUS: KOL also differs in the amidation states of residues 198, 267 and 272.
Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
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GO; GO: 0003823; F:antigen binding; TAS.
GO; GO: 0003823; F:antigen binding; TAS.
GO; GO: 0005855; P:immune response; NAS.
InterPro; IPR003006; Ig_MHC.
RinterPro; IPR003006; Ig_MHC.
Pfam; PF00147; Ig; 3.
PROSITE; PS00290; IG_MHC; 2.
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Immunoglobulin C region; Immunoglobulin domain.
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PDB: 19233; GHHU.
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Gaps 0; Length 330; 4; Indels Query Match 98.0%; Score 1729; DB 1; Best Local Similarity 97.9%; Pred. No. 1e-117; Matches 323; Conservative 3; Mismatches 4;

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378 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 407

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121 PSVFLFPPREPDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNVKTKPREEQYN 121 PSVFLFPPPREPDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYN	GVEVHNVKTKPREEQYN 180 GVEVHNAKTKPREEQYN 180	PAGE 10	AAH19337 AAH19337; AAH19337; 02-MAR-2004
181 STYRVVSVLTVIHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRD) 181 STYRVVSVLTVIHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD	VQPREPQVYTLPPSRDE 240 	TO O O	02-MAR-2004 02-MAR-2004 Hypothetical Homo sapiens
241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 	VGSFFLYSKLTVDKSRW 300 DGSFFLYSKLTVDKSRW 300		Eukaryota; Me Mammalia; Eut NCBI_TaxID=9([1]
301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330 		RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	SEQUENCE FROM TISSUE=Prima: MEDLINE=2238 Strausberg R Klausner R.D
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BAC85237; 02-MAR-2004 (TrEMBLrel. 27, Created) 02-MAR-2004 (TrEMBLrel. 27, Last sequence update) 02-MAR-2004 (TrEMBLrel. 27, Last annotation update) CDNA FLJ26298 fis, clone DMC07404, highly similar to	. 19 gamma-1 chain	* * * * * * * * * * * * * * * * * * * *	Raha S.S., Lo Bosak S.A., h Richards S., Villalon D.K.
C region. Homo sapiens (Human). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Bu Mammalia; Butheria; Primata; Catarrhini; Hominidae; Ho NCBI_TaxID=9606;	Buteleostomi; Homo.	*****	Whiting M., I Blakesley R., Rodriguez A., Krzywinski M.
[1] TISSUE=Dermoid tumor; TISSUE=Dermoid tumor; Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., St. Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Hata H., T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama T., Irie K., Otsuki T., Sagano S.; Kawakami B., Nagai K., Isogai T., Sugano S.;	H., Suzuki Y., rra M., T., Sugiyama A.,	RRRAT	"Generation of and mouse cDP proc. Natl. 7 [2] SEQUENCE FROM TISSUE=Prima.
"NEDO human cDNA sequencing project."; Submitted (UUL-2003) to the EMBL/GenBank/DDBJ databa EMBL; ALL29809; BAC85237.1; SEQUENCE 407 AA; 44159 WW; DB8E4D367B456FCE CRC6.	.ses	R B R R S	Strausberg R. Submitted (DI EMBL; BC0193: Hypothetical
Query Match Best Local Similarity 97.9%; Pred. No. 1.3e-117; Matches 323; Conservative 3; Mismatches 4; Indels	Length 407; Indels 0; Gaps 0;	Э (Ö M S	Query Match Best Local Simi
1 ASTKGBSVFPLAPSSKSTSGGTAALGGLVKDYFPEPVTVSRNSGALTSGVHTFPAVLQSS	GGALTSGVHTFPAVLQSS 60 	* & £	1 AST
61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP. 	CDKTHTCPPCEAPELLGG 120 	7	61 GLY
121 PSVFLFPPKFKDTLMISRTFBVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN	GGVEVHNVKTKPREEGYN 180 	8 6 8	121 PSV 121 PSV
181 STYRVVSVLTVLHQNWANGKEYKCKVSNKALPABIEKTISKAKVQPREPQVYTLPPR 	CYOPREPQVYTLPPSRDE 240 	3 8 8	
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301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330		₹ & ——	

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r.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

I.S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

R.F., Jordan H., Moore L., Shemen G.M., Hong L.,

R.F., Jordan H., Moore D.,

R. S., Morlan G.M.F., Carninci P., Prange C.,

en M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A., McEwan P.J., McKernan K.G., Abramson R.D., Mullahy S.J.,

S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A., McHor J.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

B.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

N., Madan A., Sodergren E.J., Lu X., Gibbs R.A.,

M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

St. Marra M.A.;

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st. Lon and initial analysis of more than 15,000 full-length human

se CDNA sequences.",
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Atheria; Primates; Catarrhini; Hominidae; Homo.
8506;
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ary B-Cells;

R.;

DEC-2001) to the EMBL/GenBank/DDBJ databases.

337; AAR19337.1; -.

1 protein.

1 protein.

464 AA; 50891 MW; 2F80673E74E2A485 CRC64;
                                         (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
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97.9%; Pred. No. 1.6e-117;
live 3; Mismatches 4;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (UUN-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (UUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BOTO3766, AAH73766.1;
InterPro; IPR003109; Ig.
InterPro; IPR0031006; Ig.
InterPro; IPR003006; Ig.Mc.
InterPro; IPR00306; Ig.V.
Ffam; PF00647; Ig. 4.
SMART; SM00409; IG. 2.
SMART; SM00406; IG. 1.
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PROSITE; PS0290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. 1.6e-117;
3; Mismatches 4;
                                                                                                                                                                                                          465 AA.
98.0%;
ilarity 97.9%;
Conservative
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TISSUE-Primary B-Cells;
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Matches 323;
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PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
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02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ26001 fis, clone DMC07585, highly similar to 1g gamma-1 chain
C region.
Homo sapiens (Human)
                                                          STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suzuki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primata, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

TISSUE=Dermoid tumor;

Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y
Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama J.
Kawakami B., Nagai K., Isogai T., Sugano S.,
"NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL: AKI29112; BAC85173.1;
EMBL: AKI2912; BAC85173.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.0%; Score 1729; DB 2; 97.9%; Pred. No. 1.6e-117; iive 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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                                                                                                                                                                                                  QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 466
                                                                                                                                                                                                                                                                                            467
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Best Local Similarity 97.9
Matches 323; Conservative
                                                                                                                                                                                                                                                                                            PRELIMINARY;
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BAC85173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
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                             02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJS6006 fis, clone DMC08725, highly similar to 1g gamma-1 chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSCALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                               Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLU27334 fis, clone TMS09201, highly similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Primata; Catarrhini; Hominidae;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                               98.0%; Score 1729; DB 2; 97.9%; Pred. No. 1.6e-117. ative 3; Mismatches 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 97.9 Matches 323; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                      SEQUENCE FROM N.A. TISSUE=Dermoid tumor;
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                                                                                                   C region.
Homo sapiens (Human)
                                                                                                                                                                   NCBI_TaxID=9606;
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Irie R., C
Sugano S.;
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BAC85175
BAC85175;
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Best Local
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Q6PJA4
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Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Jahat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I. Mang J., Hsieh F.,
A piatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Murny D.M., Sodergen B.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                        198
                                                                                                                                                                                    120
                                                                                                                                                                                                                                                          PSVFLFPPKPKDTLMISRTPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 318
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                                                                                                                                                                                                                                                                                                                 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
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                                                                                                                                                   139 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                   GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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                                                                                                                           1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                 Gaps
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Catarrhini, Hominidae, Homo.
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                                                                                                 4; Indels
"NEDO human cDNA sequencing project.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AK130844; BACS444.1;
SEQUENCE 468 AA; 51224 MW; 9280ACAD6817FC20 CRC64;
                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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                                                                   98.0%; Score 1729; DB 2; 97.9%; Pred. No. 1.6e-117; ive 3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                               QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 468
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01-OCT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                  Local Similarity 97.9
es 323; Conservative
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TISSUE=Spleen;
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                                                                   Query Match
Best Local S:
Matches 323
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BC051328; AAH51328.1;

InterPro; IPR00710; Ig-like.

InterPro; IPR003597; Ig-c1.

InterPro; IPR003596; Ig-w.

InterPro; IPR003596; Ig-w.

InterPro; IPR00406; Ig-w.

INTERPRO
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Last sequence update)
Last annotation update)
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Pred. No. 1.6e-117;
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Best Local Similarity 97.9%;
Matches 323; Conservative
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
Hypothetical protein.
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rissum=spleen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVPPKSCDKTHTCPPCPAPELLGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 260
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
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01-MAR-2004 (TEMBLE). 26, Last sequence update)
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;
Mammalla, Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                 Strausberg R., Submitted (BEC-2011) to the EMBL/GenBank/DDBJ databases. Submitted (BEC-2011) to the EMBL/GenBank/DDBJ databases. EMBL; BCO18747; AAAH18747.1; -.

InterPro: IPR0013599; Ig-11ke.

InterPro: IPR003006; Ig-11ke.

InterPro: IPR003006; Ig-Mrc.

InterPro: IPR003069; Ig-Mrc.

InterPro: IPR003069; Ig-Wrc.

Pfan; PP00047; Ig-14.

SWART; SW00409; IG: 2.

SWART; SW00409; IG: 2.

SWART; SW00409; IG: 1.

PROSITE; PSC0895; IG-IKE; 4.

PROSITE; PSC0895; IG-IKE; 4.

PROSITE; PSC0895; IG-IKE; 4.

PROSITE; PSC0896; IG-IKC; IG-IKC; IG-IKC; IG-IKC; IR-IKC; IR-IKC; IG-IKC; IR-IKC; 
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MEDIINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. 1.6e-117;
3; Mismatches 4;
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Best Local Similarity 97.9%;
Matches 323; Conservative
                                                                                                                                                                            and mouse cDNA sequences.
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TISSUE=Primary B-Cells;
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Hogoria S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Hoghins F.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Ra Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Ra Stapleton M., Soares M.B., Bonaldo M.F., Caravant T.L., Scheetz T.E., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Rachards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzarte P.H., Rathards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Rathards S., Worley V.M., Sodergren B.J., Lu X., Glibbs R.A., Rehring M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Antiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Ra Hakesley R. W., Touchman J.W., Green B.D., Dickeon M.C., Sanchez A. Bakesley R.W., Butterfield Y.S., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Rrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Schein J
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; BC053984; AAH539841; -
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_WHC.
FinerPro; IPR003596; Ig_V.
Pfam; PF00647; ig_ 1.
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SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;
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Last sequence update)
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Pred. No. 1.6e-117;
3; Mismatches 4;
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PROSITE, PS50835, IG_LIKE, 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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Proc. Natl. Acad. Sci. U.S
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FLJ26276 fis, clone DMC06522, highly similar to Ig gamma-1 chain
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Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
Kanehori K., Ishibashi T., Chiba S., Ono Y., Houta T., Watanabe M.,
Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
Sugiyama T., Irie K., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
Kawakami B., Nagai K., Isogai T., Sugano S.,
"NEDO human cDNA sequencing project ",
Sumanited (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AK130685; BAC85387.1; --
SEQUENCE 470 AA; 51642 MW; D8C41861A782293C CRC64;
                                                                                                                                                                                                                                                       Gaps
                                                                                                           Oca T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y., Hata H., Nakagawa S., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B., Narai K., Isogai T., Sugano S.; Subakami B., Nagai K., Isogai T., Sugano S.; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; ARL99787; BAC95235.1; - 460F4717D4528A16 CRC64;
                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Homo.
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CDNA FLJ27075 fis, clone SPL02093, highly similar to Ig
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Chordata; Craniata; Vertebrata;
Primata; Catarrhini; Hominidae;
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(TrEMBLrel. 27, Last seq
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                                                                                   SEQUENCE FROM N.A.
TISSUE=Dermoid tumor;
                        Homo sapiens (Human).
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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NEXUE-SPIEER;

MEDLINE=2238825; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Riabrare R.D., Collins F.S., Wagner L., Schaefer C.P.,

A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

A Richards S., Worley K.C., Hale S., Garrian G.Y., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Makesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

McTrywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

""Generation and initial analysis of more than 15,000 full-length human
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Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC062336; AAH62336.1; -.
Hypothetical protein.
SEQUENCE 470 AA; 51524 MW; CC861ACD6B7C1CC6 CRC64;
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Catarrhini; Hominidae;
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     Score 1729; DB 2;
Pred. No. 1.6e-117;
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                                                        3; Mismatches
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Mammalia, Eutheria, Primates,
     98.0%;
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                                                           Conservative
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                               Similarity
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MEDLINE-2138257; PubMed=11477912;

MILLINE-2138257; PubMed=11477912;

MILLINE-2138257; PubMed=11477912;

MILLINE-2138257; PubMed=11477912;

MILLINE-2138257; PubMed=11477912;

MILLINE ALL Schamen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Moore T., Max. I., May D., Max. I., Mang J., Haieh F.,

Moores M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley N., Modernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Whiting M.M., Madan N., Young A.C., Shevchen D.J., Lu X., Gibbs R.A.,

Milting M.M., Madan J.W., Schergen B.J., Lokson M.C.,

A Makesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,

Mones S.J., Marra M.A.;

Mones M. Madan M. M. Marra M.A.;

Mones S.J., Marra M.A.;

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                                                                                                      Gaps
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AAH14258;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria; Primates; Catarrhin; Hominidae; Homo.
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0
                                   Length 470;
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ad. Sci. U.S.A. 99:16899-16903(2002)
                                   9; DB 2;
1.6e-117;
                               ; Score 1729; DB
; Pred. No. 1.6e-
3; Mismatches
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                                      98.0%;
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                                      Query Match
Best Local Similarity
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0
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51514 MW; BFD56EF8157DBA79 CRC64;
                                          301 OOGNVFSCSVMHEALHNHYQQRSLSLSFGK 330
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  470 AA;
                                                                           Similarity
                                                                             Best Local Sim
Matches 323;
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01-MAY-2002; 2002WO-US013527.
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                                                                                                                                                                                                                                               AA019664;
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                                                                                                                                                                                                             RESULT 1
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                                                                                                                                                                                                                                        Aao19664 Human IgG
Aab04071 Zcytor 10
Aaa21960 Human IgG
Abb81641 Human IgG
Abb16736 Human Imm
Abg71856 Human Imm
Abg71856 Human Imm
Abr2205 Human Imm
Abr2205 Human Imm
Abr2205 Human Imm
Abr2205 Human Imm
Abr2206 Human A2-
Abr5836 Arti-Ang-
Aao30893 Human IgG
Ad697351 Human IgG
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Ad69505 Human IgG
Ad135055 Human IgG
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Ad135055 Human IgG
Ad135056 Human IgG
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                                                  October 27, 2004, 16:31:18; Search time 126.246 Seconds (without alignments) 937.702 Million cell updates/sec
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1 ASTKGPSVFPLAPSSKSTSG........MHEALHNHYQQRSLSLSPGK 330
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Adj95976 J
Aap91918 S
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                  2002273 segs, 358729299 residues
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Listing first 45 summaries
                                   - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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geneseqp2003as:*
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ABR39465	ABR39474	ABU08311	ABU08320	ABR39793	ABB80113	ABB80109	ADE94066	ADE94075	ADN61714	AAE35327	AAE34876	ADL15443	AD000851	AA031101	ADF11421	ADF11429	ADF11425	ADF11437	ADF11433	
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1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	1729	
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

Human, 1gG1; immunoglobulin G; immunotherapy; immune disease; Prepsilon receptor; autoimmune disease; constant region; heavy antiasthmatic; antiallardic; antiallarmametory; dermatological; antiatritic; antiathematic; antidiabetic; neuroprotective. Human IgG1 heavy chain constant region. AAO19664 standard; protein; 330 AA (first entry)

chain;

WO200288317-A2.

01-MAY-2001; 2001US-00847208. 24-OCT-2001; 2001US-00000439. ä Zhu (REGC) UNIV CALIFORNIA.

New fusion molecules comprising polypeptide sequences that bind to IgG inhibitory receptor and native IgB receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases.

Claim 64; Fig 2; 116pp; English.

The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory metif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor (FeepsilonR). Also provided are nucleotide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for treating an IgE-mediated biological response, preferably an IgE-mediated

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transgenic plant.
                                                                                                                                                                                                                                                                                                                      Sequence 330 AA;
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hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angicedema or anaphylactic shock, or autoimmune diseases such as rheumatoid arthritis, type-I diabetes mellitus, or multiple sclerosis, and for preventing of or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is the human 1gG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New cytokine receptor mouse zcytor 10, useful for detecting ligands that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand; binding; detection; modulation; recombinant cell; haematopoietic cell; lymphoid cell; myeloid cell; lymph; immune system; blood; bone; inflammatory response; inflammation; spleen; human.
                                                                                                                                                                                                                                                               121 PSVFLFFPRKPKDTLMISRTPEVICVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
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                                                                                                             100.0%; Score 1764; DB 6;
100.0%; Pred. No. 3.8e-125;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zcytor 10::IgG gamma fusion peptide.
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                                                                  heavy chain constant region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                          Query Match
Best Local Similarity 100.
Matches 330; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Presnell SR, Foster DC,
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                                                                                         Sequence 330 AA;
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AAB04071
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Isolating a nucleotide which encodes the zcytor 10 cytokine receptor enables the production of recombinant cells expressing the receptor.

Those cells can then be used to detect the presence of a modulator of zoytor10 protein by culturing the cells in the presence of a test ligand and comparing levels of activity of mouse zcytor10 in the presence and absence of the test sample. Similarly, detection of zcytor10 receptor ligand within a test sample can be achieved. The method comprising contacting a test sample containing an amino acid sequence from Cysls or Gly25 to Pro230 of the zcytor 10 cytokine receptor and detecting the binding of the polypeptide to a ligand in the sample. Specified peptide fragments of the zcytor 10 cytokine receptor and the methods described are used to identify ligands that stimulate the proliferation and/or are used to identify ligands that stimulate the proliferation and/or fragments of the cytokine receptor are useful for treating lymphoid. Immune, inflammatory, splenic, blood or bone disorders and for generating and control of an active against the receptor. A vector expressing a secreted numban zcytor 10 heterodimer is constructed. In this construct the extracellular cytokine binding domain of zcytor 10 is fused to the heteromeric contain of Igg amma and the extracellular portion of the the heteromeric contain of Igg amma and the extracellular portion of the the heteromeric contain of an inteleukin receptor subunit) is fused to human kappa light chain (See GRNESEQ record AAA54474). The two sequences are fused together using two primers (AAA54475), AAA54474).
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human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;
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stimulate proliferation or development of hematopoietic, lymphoid and myeloid cells.
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Pred. No. 1.7e-122;
3; Mismatches 4;
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                                                                                                                                                Example 17; Page 120-121; 134pp; English.
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Homo sapiens.

WO200183529-A2.

08-NOV-2001.

28-APR-2001; 2001WO-US013932

28-APR-2000; 2000US-0200298P

(PLAN-) PLANET BIOTECHNOLOGY INC.

Larrick JW, Wycoff KL;

WPI; 2002-041481/05. N-PSDB; ABA05265.

Immunoadhesin for treating human rhinovirus infection comprises chimeric intercellular adhesion molecule-1, and optionally a J chain and secretory component in association.

Disclosure; Fig 7; 138pp; English.

The invention relates to an immunoadhesin comprising: (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising a rhinovirus receptor protein linked to at least a portion of an immunoglobulin heavy chain, and (b) optionally a chain and secretory component associated with the chimeric ICAM-1 molecule. The immunoadhesin has plant-specific glycosylation and virucide activity. The immunoadhesin is useful for reducing infection by human rhinovirus (HRW) and hence the initiation or spread of the common cold by HRV. The immunoadhesin binds to HRV and reduces its infectivity, competing with cell surface ICAM-1 for binding sites, interfering with virus entry or uncoating and directing premature immunoadhesin in plants would be tetrameric, rather than dimeric. Immunoadhesin having multiple binding sites have a higher effective affinity for the virus, thereby increasing the effectiveness of the immunoadhesin. Association of secretory component and immunoglobulin J chain increases the stability of the immunoadhesin in the mucosal environment. Production is significantly less expensive in plants than in animal cell culture and production in plants is safet for human use, since plants are not known to harbor any animal viruses. The present sequence is that of a human immunoglobulin protein sequence, useful to

Sequence 330 AA;

Gaps . 0 Length 330; 4; Indels Score 1729; DB 5; Pred. No. 1.7e-122; 3; Mismatches 4; 98.08; Conservative Query Match Best Local Similarity 323; Matches

- 9 9 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFFAVLQSS 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
- 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVBPKSCDKTHTCPPCPAPELLGG 120
- 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180 121
- STYRVVSVLTVLHQNWMGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 181

240

240

- LIKNOVSLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300 241
- OCCNVFSCSVMHEALHNHYQQRSLSLSPGK 330 301

301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330

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AAE21960 RESULT

AAE21960 standard; protein; 330

AAE21960;

25-JUL-2002 (first entry)

Human death domain containing receptor (DR6) protein-related protein.

Human, therapy, death domain containing receptor; DR6; receptor; anaemia; apoptosis; rheumatoid arthritis; eczema; asthma; psoriasis; pancreatitis; diabetes; cancer; multiple sclerosis; Graves disease; glomerulonephritis; transplant rejection; systemic lupus erythematosus; hepatitis; cirrhosis autoimmune; gastritis; dermatosis; cardiopathy; infertility; haemostatic; H. pylori-associated ulceration; antiinflammatory; vasotropic; virucide; acquired immunedeficiency syndrome; AIDS; immunodeficiency virus; HIV; haemolytic uraemic syndrome; HUS; immunodeficiency; neuroprotective; adult respiratory distress syndrome; ARDS; cytostatic; thyromimetic; dermatological; hepatotropic; antibacterial

Homo sapiens.

WO200185209-A2.

15-NOV-2001.

30-APR-2001; 2001WO-US011735.

10-MAY-2000; 2000US-0203015P.

(ELIL) LILLY & CO ELI.

Song HY, Yang D; Heuer JG, Liu J, Na S,

WPI; 2002-351283/38.

Treating or preventing T cell or Th2 cell mediated condition e.g., asthma or multiple sclerosis in mammal, comprises administering composition comprising death domain containing receptor, DR6 agonist or antagonist.

Disclosure; Page 132-133; 133pp; English.

The invention relates to a method for treating or preventing a T cell mediated condition or a Th2 cell mediated condition in a mammal. The method comprising administering to the mammal a pharmaceutical composition comprising adeath domain containing receptor (DRG) agonist composition comprising a death domain containing receptor (DRG) agonist cor artagonist. The method is useful for treating or preventing a T cell mediated condition in a mammal. A DRG cagonist is useful in the manufacture of a medicament for treating or preventing at least one symptom associated with aberrant apoptosis, graft or preventing at least one symptom associated with aberrant apoptosis, graft of preventing at least one symptom associated with aberrant apoptosis, graft of preventing at least one symptom associated with aberrant apoptosis, inflammatory bowel disease, vasculitis, postiasis, pancreatitis, insulingender disease, utonimmune dermatosis, utofomatosus, autoimmune dermatosis, autoimmune gastritis, fibrosing lung cryptometors, autoimmune destricts, symptomic (TTP), chromic glomerulonephritis, heemolytic thrombocytopenic purpura (TTP), chromic glomerulonephritis, heemolytic thrombocytopenic purpura (TTP), chromic glomerulonephritis, heemolytic thrombocytopenic purpura (TTP), chromic glomerulonephritis, heemolytic chrombocytopenic purpura (TTP), chromic glomerulonephritis, heemolytic or a condition or symptom related to the above mentioned diseases in a mammal. An DRG antagonist is useful in the manufacture of a medicament of a medicament confined dispublications of infection, human immunodeficiency virus (HIV), HIV-induced lymphoma, HIV-induced acquired intentioned diseases in a infection, complications of infection, human immunodeficiency virus (HIV), HIV-induced lymphoma, HIV-induced acquired intentioned diseases in a casociated ulceration, cytoprotection during cancer treatment, a syndrome (ADDS), fullminant viral hepatitis, chronic cirrhosis, HIV-induced sequired sequired in the medicament of a utoimmune hepatitis, chronic hep

us-10-000-439-2.rag

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N-PSDB; ABQ73076
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       or
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recuperation from chemotherapy, recuperation from irradiation therapy, a condition or symptom related to the above mentioned diseases in a mammal. The present sequence is human DR6 protein-related protein
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                                                                                                                                Length 330;
                                                                                                                                                                               4; Indels
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                                                                                                                                98.0%; Score 1729; DB 5;
larity 97.9%; Pred. No. 1.7e-122;
Conservative 3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB81641 standard; protein; 330
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                                                                                                                                                Local Similarity
es 323; Conserv
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                                                                                      Sequence 330 AA;
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                                                                                                                                Query Match
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Matches
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The present invention describes an isolated human zcytor19 protein (I), and truncated zcytor19 proteins. (I) has immunosuppressive, cytostatic, antirheritic, neuroprotective, antirhlammatory, antirhermatic, antiarthritic, neuroprotective, antirhlammatory, contidabetic, nephrotropic, dermatological, anti-HIV and haemostatic activities, and can be used in vaccines. (I) or an antibody binding (I) can be used for suppressing the immune system for reducing rejection of tissue or organ transplants and grafts and for treating T-cell specific leukaemias or lymphomas and autoimmune diseases including rheumatorid arthritis, multiple sclerosis, diabetes mellitus, inflammatory bowel disease and Crohn's disease. The antibodies can also be used for treating immunologic real diseases, glomerulonephritis, mesangioproliferative disease, chronic lymphocytic leukaemia, secondary glomerulonephritis or vasculitis associated with lupus, polyarterliss, scloroderma, HIV-related diseases, amyloidosis and haemolytic uraemic syndrome. (I) and the antibodies can also be used for renal or urological neoplasms and multiple myelomas, aathma, bronchitis, emphysema and other chronic airway chain protein, which is used in an example from the present in inversion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
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Novel Zyctor19 polypeptides and polynucleotides useful for stimulating immune responses in animals for producing antibodies, and for treating autoimmune diseases, leukemia and asthma.
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antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;
muscular; lymphoid; immune; inflammatory; spleenic; blood; bone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
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98.0%; Score 1729; DB 5;
Best Local Similarity 97.9%; Pred. No. 1.7e-122;
Matches 323; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a cytokine receptor designated zcytor17. Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic, antianthritic and muscular activities. The zcytor17 proteins are useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone discrders. Agonists or anti-zcytor17 antibodies are useful in stimulating cell-andiated immunity and for stimulating lymphocyte proliferation, such as in the treatment of infections involving immunosuppression, including certain viral infections. They are also useful for inducting cytoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, pancreatings, and inflammatory bowel disease. Zcytor17 was mapped to chromosoma 5, specifically to the 5d11 chromosomal region. ABA93767 to chromosome 5, specifically to the 5d11 chromosomal region. ABA93767 to chromosome 5, specifically to the 5d11 chromosomal region. ABA93767 to chromosome 6, specifically to the 5d11 chromosomal region. ABA93767 to chromosome 6, specifically to the perseent sequences used in the
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infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; inflammatory disease; pancreatitis; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polynuclectide encoding a cytokine receptor zyctor17 which is useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.0%; Score 1729; DB 5; 97.9%; Pred. No. 1.7e-122; iive 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 17; Page 187-188; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exemplification of the present invention
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29-JUN-2000; 2000US-0214955P.
08-FEB-2001; 2001US-0267963P.
                                                                                                                                                                                                                       26-JUN-2001; 2001WO-US020484
                                                                                                                                                                                                                                                                                                                                                                                                Presnell SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                    (ZYMO.) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-090519/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 323; Conserv
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                                                                                                                                   40200200721-A2
                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                              Sprecher CA,
                                                                                                                                                                             3-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                       Maurer MF;
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The invention relates to a novel fusion protein comprising an IgE Prepsilon fragment and an IgG Fogamma fragment, which binds to an Prepsilon and an Fogamma fragment. FrogammaRIIB receptor. The fusion protein of the invention may have a use in protein therapy. The fusion protein is useful in treating or preventing IgE-mediated allergies and asthma, such as allergic asthma, allergic thinlitis, hay fever, food allergy, atopic dermatitis and drug allergy. The allergic response is particularly caused by peanut allergen. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
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                                                                                                                                                                                                                                                                                                                                                                                            Human; fusion protein; IgE Fcepsilon; IgG Fcgamma; FcepsilonRI; allergy; FcepsilonRII; FcgammaRIIB; protein therapy; IgE; IgG; asthma; hay fever; allergic asthma; allergic thinitis; hay fever; food allergy; atopic dermatitis; drug allergy; peanut allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New fusion protein which binds to FcepsilonRI or RII receptor and FcgammaRIIB receptor, useful for treating or preventing allergies and asthma, comprises an IgE Fcepsilon fragment and an IgG Fcgamma fragment.
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Pred. No. 1.7e-122;
301 QCGNVFSCSVWHEALHNHYTQKSLSLSPGK 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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/label= CH1 region
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/label= CH2_region
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/label= CH3_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 5, 32pp, English.
                                                                                                                                                                          ABP71856 standard; protein; 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the human IgG1 Fcgamma fragment
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Best Local Similarity, 97.9%;
Matches 323; Conservative
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| 114. .223
                                                                                                                                                                                                                                                                                                                                               Human IgG1 Fcgamma region.
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                                                                                                                                                                                                                                                                                                                                      fusion protein which involves identifying a candidate T-cell epitope within a junction spanning a fusion junction of a fusion protein, and changing an amino acid within the junction region to reduce the ability of the candidate T-cell epitope to interact with a T-cell receptor. The method is useful for reducing the immunogenicity of a fusion protein. It is useful for analysing, changing or modifying one or more amino acids in the junction region or protein to identify a T-cell epitope and reduce its ability to interact with a T-cell receptor. The less immunogenic fusion proteins are useful in providing threapeutic treatment. The present sequence is human immunoglobulin G1 (1991) heavy chain Fc region used to illustrate the method of the invention
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                                                                                                                           LIKNQVSLICLVKGFYPSDIAVEWESNGOPENNYKTIPPVLDSVGSFFLYSKLTVDKSRW 300
                                                                                                                                          241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
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GLYSLSSVVTVPSSSLGTQTYICNVHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                               STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                   PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
                                                                               STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reducing the immunogenicity of a fusion protein comprises changing a amino acid within the junction region to reduce the ability of the candidate T-cell epitope identified within the junction spanning to
                                                                                                                                                                                                                                                                                                                                              T-cell; immunogenic; therapy; human; immunoglobulin G1; IgG1:
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                                                                                                                                                                                                                                                                                                                        Human immunoglobulin G1 (IgG1) heavy chain Fc region.
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                                                                                                                                                                       OCGNVFSCSVMHEALHNHYQORSLSLSPGK 330
                                                                                                                                                                                    QGGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
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                                                                                                                                                ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS#NSGALTSGVHTFPAVLQSS
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ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                           GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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Sequence 330 AA,

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Length 330;
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Score 1729; DB 6;
Pred. No. 1.7e-122;
3; Mismatches 4;
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  Query Match
Best Local Similarity 97.9%;
Matches 323; Conservative
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ABR82103 standard; protein; 330 R82103

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ABR82103;

(first entry) 23-SEP-2003 Human DR6 related amino acid sequence SEQ ID NO:5

antiarthritic; antiasthmatic, dermatological; antiinflammatory; antipsoriatic; antidiabetic; ottostatic; neuroprotective; thyromimetic; antityroid; neuroprotective; thyromimetic; antitherillity; vasotropic; virucide; hepatotropic; antibacterial; antilocr; haemostatic; antianaemic; antimicrobial; anti-HIV; DR6 agonist; DR6 antagonist; immunity. Human; DR6; B-cell mediated disease; immunosuppressive; antirheumatic;

WO2003051290-A2 Homo sapiens

26-JUN-2003.

10-DEC-2002; 2002WO-US037596

17-DEC-2001; 2001US-0342632P.

(ELIL) LILLY & CO ELI

Yang Na S, Song HY, Liu J,

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Treating or preventing a B cell mediated condition e.g., chronic hepatitis or chronic cirrhosis, in a mammal by administering a pharmaceutical composition comprising a DR6 agonist or DR6 antagonist to the mammal. WPI; 2003-541604/51.

Disclosure; Page 96-97; 97pp; English.

The present invention describes a method (M1) for treating or preventing a B cell mediated condition in a mammal by administering a pharmaceutical composition comprising a DR6 agonist or DR6 antegonist to the mammal. Also described: (1) inhibiting B cell mediated immunity in a mammal, by

continistering a pharmaceturical composition of a medicament for canninistering a pharmaceturical composition of creating or preventing at least one symptom associated with conditions (Creating or preventing at least one symptom associated with conditions (Creating or preventing at least one symptom associated with conditions (CC treating or preventing at least one symptom associated with conditions (CC treating or preventing at least one symptom cannonial papersensitivity prewing a creation of the condition of transplant rejection, systemic lupus erythematosus, Behcet's disease, autoimmune nephropathy, autoimmune infertility, autoimmune pastricis, dispensional propersensitivity pneumonitis, autoimmune dermatosis, autoimmune hepatitis chonic circumine cardiopathy, autoimmune infertility, autoimmune pastricis, chronic circumine cardiopathy, autoimmune hepatitis, chronic fartility, autoimmune pastricis, chronic hepatitis, chronic circumine cardiopathy, autoimmune hepatitis, chronic hepatitis, chronic circumine the pastricis of the pastricis, chronic circumine cardiopathy, cautoimmune hepatitis, chronic hepatitis, chronic circumic consistence of autoimmune hepatitis, chronic hepatitis, chronic circumic consistence of antagonatism, chronic glomerulomephiticis, chronic hepatitis, chronic circumic consistence of antagonatism chromic circumic consistence of antagonatism chromic circumic consistence of antagonist in the manufacture of a medicament for tracting or preventing at least one symptom associated with conditions (C2) such as aberrant approach in from the hepatitis, dronic hepatitis, chronic cardiopathy, and conditions, in a mammal. DR6 has immunosuppressive, antipheratory conditions, in a mammal. DR6 has immunosuppressive, antipheratory conditions, or symptom related to the conditions, in a mammal. DR6 has immunosuppressive, antipheratory antipheratory conditions, antipheratory antipheratory conditions, antipheratory antipheratory conditions and present cardinabetic, cycocatic, munopersity, antipheratory condi administering a pharmaceutical composition comprising at least one DR6 8489999999999999999999999999999999999

Sequence 330 AA;

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 δ d à (first entry)

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New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity, hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
                                                                                                              angiopoietin-2; anorectic; cytostatic; antiarteriosclerotic; ological; antiinflammatory; osteopathic; antipsoriatic; cancer;
                                                                               Anti-Ang-2 antibody IgG1 constant region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Page 96; 161pp; English
                                                                                                                                              angiogenesis; antibody; human.
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10-OCT-2002;
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                  ABR55836;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides human antibodies that bind to stem cell factor (SCP) protein. SCF is also known as mast cell growth factor, steel factor or c-kit ligand. Antibodies of the invention are useful for preparing compositions for treating athme. They are also used in gene therapy. The present sequence is human SCF antibody heavy chain constant region
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                                                                                                                            Human, antibody, stem cell factor, mast cell growth factor, asthma, SCF, steel factor, c-kit ligand, gene therapy; heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIKNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                to stem cell factor protein, treating asthma.
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                                                                                             Human A2-G8 SCF antibody heavy chain constant region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New purified human antibody that binds useful for preparing a composition for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 10; Page 47-48; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                       Tomkinson A, Neben S;
AAO31102 standard; protein; 330 AA
                                                                                                                                                                                                                                                                         16-DEC-2002; 2002WO-US040227.
                                                                                                                                                                                                                                                                                                        17-DEC-2001; 2001US-0342174P
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            323; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     2003-523500/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 323; Conserv
                                                                                                                                                                                                                                                                                                                                      (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAL62618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 330 AA;
                                                                                                                                                                                                          WO2003051311-A2
                                                                                                                                                                             sapiens.
                                                              06-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                     Takeuchi T,
                                                                                                                                                                                                                                          26-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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2001US-0328604P 2002US-00269805

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The invention relates to a specific binding agent, which comprises at least one peptide selected from any of 62 peptides (ABR55769-830) or its fragment. The binding agents are antibodies that recognize and bind to angiopoietin-2 (Ang-2). The specific binding agent, particularly the antibody, is useful for inhibiting undesired angiogenesis, treating a cancers, inhibiting undesired angiogenesis, modulating to rinhibiting accidents, inhibiting undesired angiogenesis, modulating or inhibiting hapterating a crivity, modulating vascular permeability or plasma leakage, or treating a disease (e.g. ocular neovascular disease, obesity, haemangioblastoma, hemangioma, arteriosclerosis, inflammatory disease, inflammatory disease, inflammatory disease, atherosclerosis, endometriosis, neoplastic disease, bone-related disease, or psoriasis) in a mammal. The present sequence represents a human IgG1 constant region of an anti-Ang-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASTKGPSVFPLAPSSKSTSGGTAALGCLVXDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STYRUVSVLTVLHONWWNGKEYKCKVSNKALPAPIEKTISKAKVOPREPQVYTLPPSRDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 330 AA;
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RESULT 12 ABR55836 ID ABR55836 standard; protein; 330 AA.

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241 LIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSVGSFFLYSKLTVDKSRW 300
                                                                 301 OOGNVFSCSVMHEALHNHYOORSLSLSPGK 330
                                                                                                301 ÓQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; SEQ ID NO 2; 156pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sullivan JK,
                                                                                                                                                                                       ADF11389 standard; protein; 330 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-APR-2003; 2003WO-US010749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-2002; 2002US-0370407P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 97.9%;
Matches 323; Conservative
                                                                                                                                                                                                                                                         12-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boyle WJ, Medlock E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-845253/78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADF11388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 330 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003086289-A2.
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                        ADF11389;
                                                                                                                                                     RESULT 14
ADF11389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to cytokine fusion proteins with increased therapeutic index and methods for increasing the therapeutic index of such fusion proteins. The fusion protein comprises a non-interleukin-2 such fusion proteins. The fusion protein comparition for treating cancer, viral infections or immune disorders. The fusion protein is also used in gene therapy. The present sequence is human immunoglobulin gamma (IgG) constant region. This sequence is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                        Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder; gene therapy; immunoglobulin; Ig; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2 moiety, useful for preparing a composition for treating cancer, viral infections or immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYPPEPVTVSWNSGALTSGVHTPPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                         Human immunoglobulin gamma (IgG) 1 constant region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.0%; Score 1729; DB 6;
97.9%; Pred. No. 1.7e-122;
cive 3; Mismatches 4;
                    301 QOGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
                                         301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 51-53; 71pp; English.
                                                                                                                                        Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EMDL-) EMD LEXIGEN RES CENT CORP.
                                                                                                                                      AAO30893 standard; protein, 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-2001; 2001US-0337113P
12-APR-2002; 2002US-0371966P
                                                                                                                                                                                                                                                                                                                                                                                                                                  04-DEC-2002; 2002WO-US038780
                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 97.9
Matches 323; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-513757/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 330 AA;
                                                                                                                                                                                                                                                                                                                                                               WO2003048334-A2.
                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                        22-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                  12-JUN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gillies SD;
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                                                                                                                                                                         AAO30893;
                                                                                                     SULT 13
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241 LIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLXSKLTVDKSRW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPSPVTVSWNSGALTSGVHTFPAVLQSS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Martin F, Huang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human, antibody, osteoprotegerin ligand, OPGL, osteopenic disorder, osteopathic, antiarthritic, cytostatic, gene therapy, bone disorder, osteoporosis, bone loss, arthritis, Paget's disease, osteopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents a sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-OPGL antibody heavy chain constant region SEQ ID NO:2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elliott RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1729; DB 7;
Pred. No. 1.7e-122;
3; Mismatches 4;
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240
120
                                 120
                                                                     180
                                                                                       300
                                                                                                                                                                                                                                  241 LTKNQVSLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New immunoadhesin, useful for treating anthrax and rhinovirus, comprises chimeric toxin receptor protein linked to immunoglobulin heavy chain, and J chain and secretory component associated with the chimeric toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel immunoadhesin comprising a chimeric toxin receptor protein consisting of a toxin receptor protein linked to at least a portion of an immunoaglobulin heavy chain with a J (joining) chain and secretory component (SC) associated with the chimeric toxin receptor protein. The immunoadhesin comprises a chimeric bacterial or viral toxin receptor protein and the immunoadhesin of the invention demonstrates virucide and antibacterial activities and may be useful for reducing the binding of a viral or bacterial artigen to a host cell and thus for treating or preventing anthrax, as well as human thinovirus infection which results in the common cold. The current sequence is that of the human incommon related protein of the invention.
                    GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                   PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
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                                                                                                                                      STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoadhesin; immunoglobulin heavy chain; J chain; joining; toxin; virucide; antibacterial; anthrax; rhinovirus infection; common cold; intercellular adhesion molecule; ICAM-1; human; constant region; IGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human IgG1 heavy chain constant region protein - SEQ ID 20.
                                                                                                                                                                                                                                                                                  QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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                                                                                                                                                                                                                                                                                                                                                                                                      ADE97351 standard; protein; 330 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-OCT-2001; 2001US-00047542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-2002; 2002WO-US034197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                           Length 330;
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                                           Score 1729; DB 7;
Pred. No. 1.7e-122;
3; Mismatches 4;
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Job time : 129.246 secs
                                           Query Match
Best Local Similarity 97.9%;
Matches 323; Conservative
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Publication No. US20030082190A1
| GENERAL INFORMATION:
| APPLICANT: SAXON, Andrew
| APPLICANT: Chang, Ke
| APPLICANT: Chang, Ke
| TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
| TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES;
| CURRENT APPLICATION NUMBER: US/09/847,208;
| CURRENT PILLING DATE: 2001-05-01
| NUMBER OF SEQ ID NOS: 177
| SEQ ID NO 2
| LENGTH: 330
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Best Local Similarity 100.
Matches 330; Conservative
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CRGANISM: Homo sapiens
US-09-847-208-2
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1 ASTKGPSVPPLAPSSKSTSG.......MHEALHNHYQQRSLSLSPGK 330
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| Capta_6/ptodated/l/pubpaa/PCT_NEW PUBL.pep:*
| Capta_6/ptodated/l/pubpaa/USO6_NEW PUB.pep:*
| Capta_6/ptodated/l/pubpaa/USO6_NEW PUB.pep:*
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| Capta_6/ptodated/l/pubpaa/USO8_NEW PUB.pep:*
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| Capta_6/ptodated/l/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

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100.0%; Score 1764; DB 10; Length 330; 100.0%; Pred. No. 1.2e-128; ive 0, Mismatches 0; Indels 0;

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TYPE: PRT
ORGANISM: Homo sapiens
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US-09-995-898A-15
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Sequence 2, Application US/10000439

Publication No. US20030064063A1

GENERAL INFORMATION:
TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR TITLE OF INVENTION: FURATMENT OF IMMUNE DISEASES

FILE REFERST FILING DATE: 2001-10-24

CURRENT APPLICATION NUMBER: US/10/000,439

CURRENT FILING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1764; DB 14;
100.0%; Pred. No. 1.2e-128;
Live. 0; Mismatches 0;
                                                                                                                                    301 OQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
                                                                                                                                                          301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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No. US20030027253Alak, Julia E.
Whitmore, Theodore E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
Matches 330; Conservative,
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ORGANISM: Homo sapiens
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US-09-995-898A-15
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APPLICANT: Grant, Francis J.
TILLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
FILE SPERMANDION: CYTOKINE RECEPTOR ZCYTOR19
CURRENT APPLICATION NUMBER: US/09/995,898A
CURRENT FILING DATE: 2001-11-28
PRIOR PILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-28
PRIOR PILING DATE: 2000-01-6
PRIOR PILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FASLSEQ for Windows Version 3.0
LENGTH: 330
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| Publication No. UG20030096339A1
| GEBREAL INFORMATION
| APPLICANT: Sprecher, Cindy A. APPLICANT: Presnell, Scott R. APPLICANT: Gao, Zeren
| APPLICANT: Multimore, Theodore E. APPLICANT: Multimore, Theodore E. APPLICANT: Multimore, Toseph L. APPLICANT: Multimore, Nark F. TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTORI7 FILLE REFERENCE: 00-42
| TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTORI7 FILLE REPERENCE: 00-042
| CURRENT FILLING DATE: 2001-06-26
| PRIOR APPLICATION NUMBER: US 60/214,282
| PRIOR FILLING DATE: 2000-06-29
| PRIOR FILLING DATE: 2000-06-29
| PRIOR FILLING DATE: 2001-08-02
| NUMBER: OF SEQ ID NOS: 93
| SOFTWARE: FestSEQ for Windows Version 3:0
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ORGANISM: Homo sapiens
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181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
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Publication No. US20030166163A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
FILE REPERENCE: LEX-202
CURRENT APPLICATION NUMBER: US/10/310,719
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,113
PRIOR PILING DATE: 2001-12-04
PRIOR PILING DATE: 2001-12-04
                                                                                                                                                                                                                                                                (%) 10-269-805-68

Sequence 68, Application US/10269805

Publication Wo. US2030124129A1

Publication No. US2030124129A1

GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-72

CURRENT APPLICATION NUMBER: US/10/269,805

CURRENT PILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US 60/328,604

PRIOR PILING DATE: 2001-10-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 98.0%; Score 1729; DB 14; Best Local Similarity 97.9%; Pred. No. 6.4e-126; Matches 323; Conservative 3; Mismatches 4;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 68
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US-10-269-805-68
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US-10-310-719-8
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TYPE: PRT
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Publication No. US20020168367A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WAYCOFF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFERENCE: 030905.0004.CIP1
CURRENT APPLICATION NUMBER: US/10/047,542
CURRENT FILING DATE: 2001-10-26
PRIOR PELING DATE: 2001-10-26
PRIOR PELING DATE: 2001-04-28
PRIOR PELING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
SEQ ID NO 20
LENGTH: 330
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                                                         Length 330;
                                                                                                   Indels
                                                     Score 1729; DB 10;
Pred. No. 6.4e-126;
3; Mismatches 4;
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                                                         98.08;
                                                         Query Match
Best Local Similarity 97.99
Matches 323; Conservative
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S-10-047-542-20
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Best Local Similarity
Matches 323; Conserva
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                  -09-892-949-38
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LIKNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTIPPVLDSVGSFFLYSKLIVDKSRW 300
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Sequence 81, Application US/10320231A
| Sequence 81, Application US/10320231A
| Sequence 81, Application No. US20030194405A1
| Publication No. US20030194405A1
| Publication No. US20030194405A1
| APPLICANT: Noben, Steven
| APPLICANT: Takeuchi, Toshiniko
| APPLICANT: Takeuchi, Toshiniko
| TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For TITLE OF INVENTION: Treatment Of Asthma
| TITLE OF INVENTION: Treatment Of Asthma |
| FILE REFERENCE: 7430*463 |
| CURRENT APPLICATION NUMBER: US/10/320,231A |
| PRIOR APPLICATION NUMBER: US 60/342,174 |
| PRIOR APPLICATION NUMBER: US 60/342,174 |
| SOFFWARE: Patentin Version 3.2 |
| SOFFWARE: Patentin Ver
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                 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
                                                61 GLYSLSSVVIVPSSSLGTQTYICNVNHKPSNTKVDKKVJPKSCDKTHTCPPCPAPELLGG 120
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ORGANISM: Homo sapiens
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Publication Wo. US2030166877A1
GAPBLICANT: Gillies, Stephen
TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
FILE REFRENCE: LEX-017
CURRENT APPLICATION NUMBER: US/10/112,582
PRIOR APPLICATION NUMBER: US 60/280,625
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Version 3.0
SEQ ID NO 1
LENGTH: 330
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; OTHER INFORMATION: human Ig gamma heavy chain C region
US-10-112-582-1
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PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 330
TYPE: PRT
ORGANIEM: Home sapiens
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ORGANISM: Homo sapiens
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NAME/KEY: misc
LOCATION: (1)..(
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APPLICANT: AN Wenfeng
APPLICANT: No. US2004002922BAlak, Julia E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Grant, Francis J.
APPLICANT: Kindsvogel, Wayne R.
APPLICANT: Kindsvogel, Wayne R.
APPLICANT: Kindsvogel, Wayne R.
TITLE OF INVENTION: CYTOKINE RECEPTOR
TITLE REFERENCE: 02-10
CURRENT APPLICATION NUMBER: US/10/420,034A
CURRENT FILING DATE: 2003-04-18
PRIOR FILING DATE: 2002-04-19
NUMBER OF SEQ ID NOS: 69
SEQ ID NO 15
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Publication No. US20040029228A1
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Matches 323; Conservative
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ORGANISM: Homo sapiens
                               ORGANISM: Homo sapiens
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Best Local Simi
Matches 323;
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TYPE: PRT
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Publication No. US20040023313A1
Publication No. US20040023313A1
APPLICANT: Boyle, William
APPLICANT: Bliot, Malchun
APPLICANT: Bliot, Robin
APPLICANT: Bliot, Robin
APPLICANT: Bliot, Robin
APPLICANT: Matlin, Francis
APPLICANT: Matlin, Francis
TITLE OF INVENTION: Inhibitors
TITLE OF INVENTION: Inhibitors
FILE REPERSING: MBHB 01-1145-A
CURRENT APPLICANTON NUMBER: US/10/408,901
CURRENT APPLICANTON NUMBER: US/10/408,901
CURRENT PILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 330
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OTHER INFORMATION: synthetically generated plasmid sequence:-10-383-902A-6
                                                   Publication US/10383902A
Publication No. US20030224408A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
APPLICANT: Mallberg, Jurgen
APPLICANT: Ladner, Robert C.
APPLICANT: Ladner, Robert C.
TITLE OF INVENTION: LIGAND SCREENING AND DISCOVERY
FILE REFERENCE: 10280-42001
CURRENT FILING DATE: 2003-007
PRIOR MANUEL PRACTICATION NUMBER: BASISEQ for Windows Version 4.0
SEQ LING SEQ IN NO.
SEQ SOFTWARE: FASISEQ for Windows Version 4.0
SEQ TYPE: PRT
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APPLICANT: Vezina, Chris
APPLICANT: Wong, Lu Min
APPLICANT: Qian, Xueming
TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
FILE REFERENCE: 01,1554
CURRENT APPLICATION WUMBER: US/10/656,769
CURRENT FILING DATE: 2003-09-05
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin version 3.0
EDO ID NO 2
LERGARE - 2
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APPLICANT: Presnell, Scott R.
APPLICANT: Gao, Zeren
APPLICANT: Whitmore, Theodore E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Whitmore, Marker.
ITILE OF INVENTION: CYTOKINE RECEPTOR ZCYTORIT
FILE REFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/10/772,531
CURRENT FILING DATE: 2004-02-05
FRIOR FILING DATE: 2001-06-26
FRIOR FILING DATE: 2001-06-29
FRIOR FILING DATE: 2001-06-36
FRIOR FILING DATE: 2001-06-36
FRIOR FILING DATE: 2001-08-02
FRIOR FILING DATE: 2001-08-03
FRIOR FILING DATE: 2001-08-02
FRIOR FILING DATE: 2001-08-03
FRIOR FILING DATE: 2001-08-02
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ORGANISM: Homo sapiens

US-10-656-769-2
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APPLICANT: Liu, Jingi
APPLICANT: Liu, Jingi
APPLICANT: Na, Songing
APPLICANT: Song, Ho Yeong
APPLICANT: Song, Ho Yeong
APPLICANT: Yang, Derek Di
TITLE OF INVENTION: TREATING T-CELL MEDIATED DISEASES BY MODULATING DR6 ACTIVITY
FILE REFERENCE: X-13992
CURRENT FILING DATE: 2002-10-16
NUMBER OF SEQ ID NOS: 5
SOFTWARER: Patentin version 3.0
SEQ ID NO 5
LENGTH: 330
                                                                                                                                                                                                                                  241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
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Pred. No. 6.4e-126;
3; Mismatches 4;
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Publication No. US20040043022A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-257-907-5
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Matches 323;
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TYPE: PRT ORGANISM: Homo sapiens

Sequence 2, Application US/10656769
Publication No. US20040097712A1
GENERAL INFORMATION:
APPLICANT: Varnum, Brian
APPLICANT: Witte, Alison

US-10-656-769-2

-10-772-531-38

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                                                                                                                                                 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
                                                                                                                                                                                                                                               181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
                                                                                                                                                                                                                                                                                                                        241 LTKNQVSLTCLVKGFVPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRM 300
241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKKRN 300
                                                                       0; Gaps
Query Match 98.0%; Score 1729; DB 16; Length 330; Best Local Similarity 97.9%; Pred. No. 6.4e-126; Matches 323; Conservative 3; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
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Sequence 16, Appl
Sequence 53, Appl
Sequence 7, Appli
Sequence 17, Appli
Sequence 12, Appli
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Sequence 14, Appli
Sequence 16, Appli
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Sequence 17, Appli
Sequence 18, Appli
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Sequence 16,
Sequence 53,
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1 ASTKGPSVFPLAPSSKSTSG......MHEALHNHYQQRSLSLSPGK 330
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(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-09-382-561A-16

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ALIGNMENTS

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ZZIP: 94080

ZZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,311

TILING DATE: 02-VAY-1994
CLASSIFICATION WHERE: US/08/236,311

APPLICATION WHERE: US/08/236,311

APPLICATION WHERE: US/08/236,311

APPLICATION WHERE: US/08/277

FILING APPLICATION DATA:
APPLICATION NUMBER: US/250785

FILING APPLICATION DATA:
APPLICATION NUMBER: US/250785

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FILING APPLICATION UNFORWATION: US/250785

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FILING APPLICATION UNFORWATION: US/250785

FILING APPLICATION OF AURICATION: US/250785
                                                               Sequence 7, Application US/08236311
Patent No. 5565335
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
ITTLE OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Prancisco
STATE: California
RESULT 1
US-08-236-311-7
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LENGTH: 371 amino acids TYPE: amino acid TOPOLOGY: linear

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US-10-157-408-7
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                                                                                                                           1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALISGVHTFPAVLQSS
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                                            DB 1; Length 371;
                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-JUN 1995
CLASSIFICATION: 435
PRIOR APPLICATION ATA:
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
FILING DATE: 02-MAY-1994
PRIOR APPLICATION NUMBER: 07/936190
                                      Query Match
98.0%; Score 1729; DB 1,
Best Local Similarity 97.9%; Pred. No. 3e-157;
Matches 323; Conservative 3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STRES: South San Francisco
CITY: South San Francisco
STATE: California
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08457918
Patent No. 6117655
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 371;
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PATENT NPORMATION:
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
ITILE OF INVENTION: Addreson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEES: Generalecch, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Prancisco
STRATE: California
COUNTRY: USA
ITP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy dising COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM SYSTEM:
COMPUTER: IBM PC compatible
COMPUTER: IBM SYSTEM:
COMPUTER: IBM PC compatible
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Pred. No. 3e-157;
3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-UTN-1995
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 07/936190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/157,408 FILLING DATE: 28-May-2002 CLASSIFICATION: 435
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CURRENT APPLICATION DATA:
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P04,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415,725-981
TELERAX: 415,725-981
TELEX: 910,731-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
             36,575
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Best Local Similarity - 97.9%;
Matches 323; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 STYRVVSVLTVLHQNWANGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 LTKNÓVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 101
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Best Local Similarity 97.9%; Pred. No. 3e-157;
Matches 323; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Glorich, Roger
APPLICANT: Link, Brian
APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
APPLICATION NUMBER: 07/84277
PILING DATE: 18-FEB-1992
APPLICATION NUMBER: 07/260785
FILING DATE: 28-EEP-1988
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REGISTRATION NUMBER: 36,575
REGISTRATION NUMBER: 96,444PIC3
TELERCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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Patent No. 6129914
                                                                                                                                                                                                                                                                                                                TELEFAX: 415/952-9881
TELEX: 910/311-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                     YPE: amino acid
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117 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 PSVFLFPPKRDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
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| Patent No. 5777085
| GENERAL INFORMATION:
| APPLICANT: Tso, Man Sung
| APPLICANT: Tso, J. Yun
| TITLE OF INVENTION: Humanized Antibodies Reactive with
| TITLE OF INVENTION: GPIIB/IIIA
| NUMBER OF SEQUENCES: 23
| CORRESPONDENCE ADDRESS: Milliam M. Smith
| STREET: One Market Plaza, Steuart Tower, Suite 2000
                OPPERATING SYSTEM: PC-DOS/MS-DOS
COOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR.1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, william M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

98.0%; -Score 1729; DB 3;
Best Local Similarity 97.9%; Pred. No. 3.9e-157;
Matches 323; Conservative 3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                    011823-004901
IBM PC compatible
                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2420
TELEPAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 446 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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US-08-458-516-13
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PSVFLFPPKFKDTLMISRIPEVTCVVVDVSHEDPEVKFWWYVDGVEVHNAKTKPREEQYN 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STYRVVSVLIVLHONWMNGKEYKCKVSNKALPAPIEKTISKAKVOPREPOVYTLPPSRDE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STYRVVSVLTVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIKNQVSLICLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSVGSFFLYSKLIVDKSRW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVBPKSCDKTHTCPPCPAPELLGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.0%; Score 1729; DB 4; 97.9%; Pred. No. 4.2e-157; cive 3; Mismatches 4;
                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 5.25 inch, 360 KD COMPUTER: IBM AT COMPATIBLE OF SPEATING SYGTEM: PC-DOS/NG-DOS V 3.2 SOFTWARE: WordPerfect 5.0 (Dos Text) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/030,175 FILING DATE: 17-MAY-1993
CLASSIFICATION: 42 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01578
FILING DATE: 13-SEP-1991
ATONNEY AGENT INFORMATION:
NAME: ETTSK, Barbara G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1768-113
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: 1'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (202) 783-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 97.9
Matches 323; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-08-030-175-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-030-175-42
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Patent No. 6767996

GENERAL INFORMATION:
PAPLICANT: Gorman, Scott D. APPLICANT: Gorman, Scott D. APPLICANT: Clark, Michael R. APPLICANT: Waldmann, Herman TITLE OF INVENTION: ATTERED ANTIBODIES AND THEIR PREPARATION NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:
STREET: 555 13TH SI., NW Suite 701 East
CITY: Washington
CITY: Washington
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 98.0%; Score 1729; DB 1; Length 4
Best Local Similarity 97.9%; Pred. No. 4e-157;
Matches 323; Conservative 3; Mismatches 4; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTONNEY/AGENT INPORMATION:
NAME: SMITH, William M.
REGISTRATION NUMBER: 30,223
REBERNICE/DOCKET NUMBER: 30,223
REBERNICE/DOCKET NUMBER: 31,223
REBERNICE/DOCKET NUMBER: 31,223
RELEFRATION NUMBER: 31,223
RELEFRATION FOR SEQ 1D NO: TELEFRANCE 415-326-2400
TELEFRANCE GLARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
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US-08-030-175-41
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TOPOLOGY:
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STYRUVSVLTVLHONWMNGKEYKCKVSNKALPAPIEKTISKAKVOPREPOVYTLPPSRDE 240
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COMPUTE: 2004

ZIP: Z004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage computer: IBM AT compatible OPERATING SYSTEM: PC-DGS/MS-DOS V 3.2

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/030,175

ZILING DATE: 17-MAY-1993

CLASSIFICATION NUMBER: PCT/GB91/01578

FILING DATE: 13-SEP-1991

APPLICATION NUMBER: 90.377

REGESTRATION NUMBER: 1769-113

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
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1.08-378-939-10
20-08-378-939-10
Sequence 10, Application US/08378939
Sequence 10, Application US/08378939
Settent No. 5876961
GENERAL INFORMATION:
APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, JAMES SCOTT
APPLICANT: LEWIS, JAMEN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE
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97.9%; Pred. No. 4.2e
tive 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 467 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 97.9
Matches 323; Conservative
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241 LIKNQVSLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPBLLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN
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COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION: 435
PRIOR PAPLICATION: A35
PRIOR DATE:
CLASSIFICATION: A35
PRIOR DATE:
CLASSIFICATION: A35
PRIOR DATE:
APPLICATION NUMBER: US 07/952640
FILING DATE: 0.-DEC-1992
ATTORNEY/AGENT INPORMATION:
NAME: BRNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 30,377
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: (202) 783-6040
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: (202) 783-6040
TELECOMMUNICATION NUMBER: (202) 783-6040
TELECOMMUNICATION NUMBER: US 010:
SEQUENCE CHARACTERISTICS:
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; Sequence 54, Application US/09746359A
; Datent No. 6610286
; GENERAL INFORMATION:
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Chandrasekher, Yasm
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Madden, Karen L.
Kelly, James D.
Sprecher, Cindy A.
Blumberg, Hal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Thompson, Penny
APPLICANT: Foster, Donald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 476 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 323; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-378-939-10
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240

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GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 357
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                                                                                                                                                                                                                                                                                                                                                                                                                 242 ASTROPSVFPLAPSSKSTSGGTAALGCLVKDYFPBPVTVSWNSGALTSGVHTFPAVLQSS 301
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                   Query Match

98.0%; Score 1729; DB 4; Length 567;
Best Local Similarity 97.9%; Pred. No. 5.6e-157;
Matches 323; Conservative 3; Mismatches 4; Indels
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APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: O. 6610266ak, Julia B.
TILE REFERENCE: 99-108
CURRENT APPLICATION NUMBER: US/09/746,359A
CURRENT PILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/11,969
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/213,341
PRIOR APPLICATION NUMBER: 60/213,341
PRIOR APPLICATION NUMBER: 60/213,341
SPRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 3.0
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98.0%; Score 1729; DB 4;
Best Local Similarity 97.9%; Pred. No. 5.7e-157;
Matches 323; Conservative 3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Madden, Karen L.
Kelly, James D.
Sprecher, Cindy A.
Blumberg, Hal
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Foster, Donald C.
Xu, Wenfeng
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ORGANISM: Homo sapiens
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US-09-746-359A-53
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; OTHER INFORMATION: soluble zalphallR/IgGgammal polypeptide
ys-09-825-561A-16
                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
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APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: No. 6773394K, Julia E.
APPLICANT: No. 6773394K, Julia E.
APPLICANT: Nest, James W.
APPLICANT: Nestenell, Scott R.
APPLICANT: Helly, Richard D.
APPLICANT: Helly, Andrew J.
APPLICANT: No. 22
CURRENT PRISON, SOLUBLE ZALPHALI CYTOKINE RECEPTORS
FILE REFERENCE: 00.22
CURRENT APPLICATION NUMBER: US 60/194;731
PRIOR APPLICATION NUMBER: US 60/194;731
PRIOR APPLICATION NUMBER: US 60/194;731
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SEQ ID NO 16
LENGTH: S67
TITLE OF INVENTION: Method for Treating Inflammation
                                                                                                                                                                                                                                                                                                                                                                  98.0%; Score 1729; DB 4;
97.9%; Pred. No. 5.3e-157;
iive 3; Mismatches 4;
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              FILE REFERENCE: 99-108
CURRENT APPLICATION NUMBER: US/09/746,359A
CURRENT APPLICATION NUMBER: US/09/746,359A
CURRENT FILING DATE: 2001-05-21
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
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; Sequence 16, Application US/09825561A
; Patent No. 6777539
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ORGANISM: Artificial Sequence
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Best Local Similarity 97.9°
Matches 323; Conservative
                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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Patent No. 6537809
GENERAL INFORMATION:
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                                                                            STYRVVSVLTVLHQNWMGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
                                                                                                  LTKNOVSLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
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Patent No. 6472179
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: ADD USING
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT FILING DATE: 1990-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR PLING DATE: 1999-05-19
PRIOR PLING DATE: 1999-05-19
PRIOR PLING DATE: 1999-05-39
NUMBER OF SEQ ID NOS: 32
SUSTRANE: FASTSEQ for Windows Version 3.0
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Pred. No. 1.2e-156;
3; Mismatches 4;
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Best Local Similarity 97.9%;
Matches 323; Conservative 3
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3-09-313-942-9
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LENGTH: 951
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121
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Sequence 7, Application US/09289942A

3SULT 13 3-09-289-942A-7

APPLICANT: BRAMS, PETER
APPLICANT: BRAMS, PETER
TITLE OF INVENTION: BPETERING HIGH APPINITY HUMAN MONOCLONAL ANTIBODIES
TITLE OF INVENTION: SPECTRIC TO RSV F-PROTEIN AND METHODS FOR THEIR
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
TOURRENT APPLICATION NUMBER: US/09/140,002
CURRENT FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
SOFTWARE: PALENTIN VEF: 2.1
SEQ ID NO 27
LENGTH: 475
LENGTH: 475
LENGTH: 475 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120 121 PSVFLFFPKPKDTLMISRTPEVTCVVVDVSHEDFEVKFNWYVDGVEVHNVKTKPREEQYN 180 313 STYRVVSVLTVLHQDWLNGKEYKCKVSNKAFPAPIEKTISKAKGQPREPQVYTLPPSRDE 372 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300 373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 432 253 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 312 APPLICANT: Pai, Emil F.
APPLICANT: Pai, Emil F.
APPLICANT: Riein, Michel H.
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
TITLE OF INVENTION: Fab'-EPITOPE COMPLEX FROM THE HIV-1 CROSS-NEUTRALIZING
TITLE OF INVENTION: MONOCLONAL ANTIBODY 2F5
FILE REFERENCE: 1038-926 MIS-jb
CURRENT APPLICATION NUMBER: US/09/289,942A
CURRENT FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 9
SOSTWARE: Patentin Ver. 2.1
SEQ ID NO 7 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 193 GLYSLSSUVTVPSSSLGTQTYICNVNHKPSN1KVDKKVEPKSCDKTHTCPPCPAPELLGG 181 STYRVVSVLTVLHQNWNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 0; DB 4; Length 462;

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TITLE OF INVENTION: "MONNEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "MONNEY MONOCLONAL AND B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: TO HUMBURIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STREET: VA
COUNTRY: USA
                                                                                                          205
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                                                                                                                                                                                                                 PSVFLPPPKPKDTLMISRTPEVICVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
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tch 97.8%; Score 1725; DB 4; Length 475; al Similarity 97.6%; Pred. No. 1e-156; 322; Conservative 3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                      301 QOGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08487550
Patent No. 6113898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.8%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
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5.1.6 Compugen Ltd.		; Search time 20.2278 Seconds (without alignments) 1103.547 Million cell updates/sec	MHEALHNHYQQRSLSPGK 232			ers: 283416			*	s predicted by chance to have a. e score of the result being printed, total score distribution.	-		gamma-1 chain	ig neavy chain v r	Ig gamma-3 chain C	19 gamma-3 chain C Ig gamma-3 heavy c	Ig gamma-2 chain C Ig gamma-4 chain C	Ig gamma chain C r Ig gamma 2b chain	Ig gamma 2a chain Ig gamma 4 chain c	Ig gamma-2 chain C Ig gamma 1 chain c	Ig gamma 3 chain c Ig heavy chain pre	Ig gamma-2b chain Ig gamma-3 chain C	Ig heavy chain C r	IN SEMENT TO COLUMN TO COL	Ig gamma-1 chain C	Ig gamma-1 chain C	Ig gamma-2c chain Ig gamma-2a chain Ig qamma-2a chain	1
GenCore version 5 Copyright (c) 1993 - 2004 Co	4 protein - protein search, using sw model	04, 16:51:09	itle: srfect score: 1260 squence: 1 BPKSCDKTHTCPPCPAPELL	oring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	earched: 283416 seqs, 96216763 residues	otal number of hits satisfying chosen parameters	inimum DB seq length: 0 iximum DB seq length: 2000000000	<pre>>>st-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries</pre>	<pre>itabase : PIR 79:*</pre>	Pred. No. is the number of results predic score greater than or equal to the score and is derived by analysis of the total a		smult Query No. Score Match Length DB ID	1225 97.2 330 1	1217 96.6 255 4	1138 90.3 377 2	1123 89.1 289 1	1107 87.9 326 1 1097 87.1 327 1	868.5 68.9 328 2	868.5 68.9 328 2 865 68.7 277 2	858 68.1 329 1 847.5 67.3 328 2	840.5 66.7 328 2 820 65.1 470 2	813 64.5 333 2 812.5 64.5 329 1	811.5 64.4 308 2	801.5 63.6 398 1 704 5 63.1 444 2	789.5 62.7 324 1	784.5 62.3 393 1	21 7/6.5 61.6 329 2 500847 28 776 61.6 330 1 G2MSA 29 776 61.6 469 2 537483	

Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain		Ig gamma-2a chain		D		gamma heavy	heavy	heavy chain	Ig gamma-1 chain C	Y heavy	Ig heavy chain pre	Ig mu chain C regi	Iq mu chain C regi
G2MSAB	G2MSAM	840295	G2MS11	PS0019	G2MSBM	806611	S01321	146732	569340	A36040	S14236	B46529	S04845	\$25644	MHMS
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ALIGNMENTS

RESULT 1 GHHU Ig gamma-1 chain C region - human	C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004 C.Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146 R.Ellison, J.W.; Berson, B.J.; Hood, L.E.	Nucleic Acids Res. 10, 4071-4079, 1982 A;Fille: The nucleotide sequence of a human immunoglobulin C-gammal gene. A;Reference number: A93433; MUID:82274238; PMID:6287432 A;Accession: A94433 A;Molecule type: DNA	PO1857; EMBL:Z17 he Glm(17) alloty after translation	7 A A T	R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T. Cell 29, 671-679, 1982 A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a c A;Reference number: S33887; MUID:83001943; PMID:6811139 A;Accession. S33887 A;Molecule type: DNA A;Residues: 88-113;235-330 <tax></tax>	A;Cross-references: EMBi:217370 K;Cunningham, B.A.; Rutlashauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, (Biochemistry 9, 3161-3170, 1970 A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequency A;Reference number: A90563; MUD:71064024; PMID:5489771 A;Contents: myeloma protein Eu A;Accession: B90563	A; Molecule type: protein A; Mosidus: 1-96, R', 98-135 < CUN> A; Residuss: 1-96, R', 98-135 < CUN> A; Note: this sequence has the Glm(3) marker, 97-Arg A; Note: this sequence has the Glm(3) B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M. Biochemistry 9, 3171-3181, 1970 A; Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequer A; Reference number: A90564; MUID:71064025; PMID:5530842 A; Contents: Eu	A; Accession: A90564 A; Molecule type: protein A; Residues: 136-154, (2, 156-165, (2, 167-176, (2', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,' A; Note: this sequence has the Gim(non-1) markers, 239-Giu and 241-Met R; Ponstingl, H.; Hilschmann, N. R; Ponstingl, H.; Hilschmann, N. A; Physioll. Chem. 357, 1571-1604, 1976 A; Title: Die Primeerstruktur eines monoklonalen Iqq1-Immunglobulins (Myelomprotein Nie),
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A; Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease. A; Reference number: $69339; MUID:95262687; PMID:7744049
A; Accession: $63339
A; Status: preliminary
A; Residues: preliminary
A; Rolecule type: mRNA
A; Residues: 1-374 < KGHA>
A; Cross-references: EMBL:X81695
A; Cross-references: EMBL:X81695
A; Residues: 1-374 < KGHA>
A; Reference number: $72664
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CySpecies: synthetic

A,Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli

A,Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli

C,Date: OG-Jan.1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000

C,Accession: S3186

R,Fiblula, D.

A,Description: Screaing method for protein-protein interactions of cloned gen

A,Reference number: S31866

A,Reference number: MANA

A,Residues: 1-255 FILL>

A,Residues: 1-255 FILL>
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C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;2-25/Region: human Ig gamma-1 chain C region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Residues: 1-140, C', 142-374 «KH2»
A.Cross-references: BMBL:X81695
C.Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
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Pred. No. 1.2e-84;
5; Mismatches 4;
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Pred. No. 1e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 96.1%;
Matches 223; Conservative
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ilarity 96.6%;
Conservative
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                                                                                                                                                         A; Molecule type: protein
A; Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A; Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A; Nother this sequence has the Gim(17) and Gim(1) markers
R; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-47, 1983
A; Title: Dhe Primarestruktur des Kristallisierbaren monoklonalen Immunglobulins IgG1 KOI
A; Reference number: A91023; MUID: 8328911; PMID: 8848994
A; Contents: myeloma protein KOL; disulfide bonds
A; Rocession: A91723
A; Molecule type: protein
A; Residues: 1-96, 'R', 98-197, 'D', 199-238,'E', 240,'M', 242-266,'D', 268-271,'D', 273-330 <SCH
A; Redelmes: 1-96, 'R', 98-197,'D', 199-238,'E', 240,'M', 242-266,'D', 268-271,'D', 273-330 <SCH
A; Redelmes: 1-96, 'R', 98-197,'D', 199-238,'E', PMID: 4923144
A; Reference number: A90565; MUID: 71064027; PMID: 4923144
A; Ribre covalent structure of antibody structure of monoclonal IgG1 immunoglob
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A; Teleference number: A91667; MUID: 77070267; PMID: 1002129
A; Contents: annotation; disulfide bonds
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Map position: 14q32.33-14q32.33
A;Map position: 14q32.33-14q32.33
A;Map position: 14q32.33-14q32.33
A;Map position: 194/1 114/1; 224/1
B;Cromplex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c;Complex: An immunoglobulin heterotetramer; immunoglobulin cregion; immunoglobulin homology
C;Superfamily: immunoglobulin homology cimi>
F;20-84;Domain: immunoglobulin homology cimi>
F;313-206;Domain: immunoglobulin homology cimi>
F;343-310,Domain: immunoglobulin homology cimi>
F;343-310,Domain: immunoglobulin homology cimi>
F;37-83,144-204,250-308/Disulfide bonds: #status experimental
F;105,112;Disulfide bonds: interchain (to heavy chain) #status experimental
F;106,Binding site: carbohydrate (Asn) (covalent) #status experimental
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C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S63339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                               A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
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Matches 225; Conserv
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A; Molecule type: protein
A; Mesidues: 1-289 «FRA»
A; Mostes: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
A; Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
A; Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 con
A; Note: the sequence of residues 42-76 was taken from the reference that follows
B; Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
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                                                                                                                                                                                                                                        266 ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig gamma-3 chain C region, form LAT - human (Species: Homo sapiens (man) (C)Species: Homo sapiens (man) (C)Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004 (C)Accession: A60764 (PACCESSION: A60764 (PACCESSION: A60764) (PACCESSION: A60764) (PACCESSION: A60764) (PACCESSION: A) (
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C;Species: Homo sapiens (man)
C;Date: 31-Dec-1979 #sequence revision 23-Oct-1981 #text_change 16-Jul-1999
C;Accession: A80442; A92219; A90198; A93915; A02149
C;Accession: A80442; A92219; A90198; A93915; A02149
Biochemistry 19, 4304-4308, 1980
A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: SA;Tetle: Primary structure of human gamma3 immunoglobulin deletion mutant: A;Cottents: heavy chain disease protein Wis
                                                                                             206 KWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                               ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
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                                        61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
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89.7%; Pred. No. 2.1e-78;
tive 11; Mismatches 13;
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Best Local Similarity 89.7%
Matches 208; Conservative
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A;Molecule type: DNA
A;Residues: 1-377 <HUC>
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Species: Homo sapiens (man)
Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
Accession: A23511
Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: Reference number: A23511; MUID:86148507; PMID:3081877
Accession. A23511
Accession. A23511
Residues: 1-377 <HUC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                         gramma chain C region - chimpanzee ; Species: Pan troglodytes (chimpanzee); Jabte: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999; Accession: P70207 ; Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L. J. Immunol. 28, 319-322, 1991; Title: Nucleotide sequence of chimpanzee Fc and hinge regions. ;Reference number: P70207; MUID:91287716; PMID:2062315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BPKSCDTTHTCPPCAAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                            204 PVLDSDGSFF1YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRS 225
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Gross references: GDB:119339; CMIM:147120
:Map position: 14432.33-14432.33-14533.
:Introns: 99/3; 115/3; 130/3; 145/3; 160/3; 270/3
:Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1172; DB 2; Length 2:
Pred. No. 2.3e-81;
4; Mismatches 6; Indels
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89.7%; Pred. No. 1.5e-78;
iive 11; Mismatches 13;
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Best Local Similarity 95.6%;
Matches 215; Conservative
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nes 208; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-234 <EHR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: mRNA:
Residues: 1-234 <EHI
181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146
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A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; I A;Note: Lys-326 is probably removed posttranslationally
B;Namay, A.C.; Tung.
B;Namay, A.C.; Tung.
B;Namiol. 125; 1048-1054, 1380
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and 1 A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809 protein
A;Residues: 1-19, (0', 21-57, 2', 59, 'A', 61-193, 'D', 195-325 < WAN>
A;Note: Trp-156 is at or near the complement-binding site
A;Note: Trp-156 is at or near the complement-binding site
A;Note: Trp-156 is at or near the complement-binding site
A;Note: Trp-156 is at or near the complement-binding site
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A;Note: Trp-156 is at or near the complement-binding site
A;Note: Trp-156 is at or near the complement-binding site
A;Note: Trp-156 is at or near the complement and acid sequences of the three heavy chain constant region domains of a A;Reference number: A93132; MUID:801357; PMID:118920
A;Note: this sequence has since been revised
A;Note: this sequence has since been revised
A;Note: this sequence has maino acid sequence of residues 381-391 of human immunoglobulin g
A;Reference number: A93132
A;Reference number: A934591
                                    GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; i posttranslationally
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A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kind position: 14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.33-14q32.34-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32.31-14q32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, .
A;Note: the revised sequence differs from that shown in having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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88.4%; Pred. No. 2.8e-76;
iive 12; Mismatches 11.
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                                                                                                                                                                                                                                                                                                                                                A,NOTE: The Inige region in gamma-3 chains is about four times as 10ng as in other gamma due segment (12-28)
A,NOTE: Creatines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter R,Nolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A,Title: The manno acid sequence of "heavy chain disease" protein ZUC. Structure of the A,Reference number: A90189, MUDD:77021516; PMID:822945
A,Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues A,Rocession: A90189, MUDD:77021516; PMID:822945
A,Contents: heavy chain disease protein Zuc, partial of the CHI region, and part of the A,Residues: 59-125, EB,128-226,228-289 (NOL)
A,Residues: 59-125, EB,128-226,228-289 (NOL)
A,Roce: this protein lacks most of the V region, all of the CHI region, and part of the R,Adexander, A.; Steinmez, M.; Barithalit, D.; Frangione, B.; Franklin, E.C.; Hood, L.; Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A,NOTE: this protein lacks most of the V region, and part of the A,Reference number: A33915, MUD:82247335, PMID:6608505
A,Contents: heavy chain disease protein Own
A,Reference number: A33915, MUD:82247335, PMID:6608505
A,Contents: heavy chain disease protein Pis is shown.
C,Geneiue: 12-70;72-114;116-1125, EZ,127-133, LZ,135-136, EZ,138, YY,140-154, PD, 156-157
A,NOTE: this sequence may represent an allelic form or another gamma chain subclass C,Geneiues: 12-70;72-133, 144;116-125, EZ,127-133, C,MMID: A,MMID: A)Reference number: A92219; MUID:77118561; PMID:402363
A)Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of nrotain a by Accession: A92219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30.-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: Ap3906, Ap2809; Ā90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy (A;Reference number: A93906; MUID:82197621; PMID:6804948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 KWYYDGVQVHNAKTKPREQQENSTFRVVSVLTYLHQNWLDGKEYKCKVSNKALPAPIEKT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                      A,Molecule type: protein
A,Residues: 12-97 <MIC>
A,Note: the hinge region in gamma-3 chains is about four times as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPG 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-326 <ELL>
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225 SLSLSPGK 232
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                                                                                                                                                A; Accession: A91749
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the subunits associate into
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CPSCPAPEFLGGFSVFLFPFKFKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVH 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPRE 130
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1240-307/Domain: immunoglobulin homology <IM3>
1240-317/Domain: immunoglobulin homology <IM3>
1240-1241-1241-124-125/Disulfide bonds: #status predicted
127-83.141-201.247-305/Disulfide bonds: #status predicted
106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
177/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                               Species: Homo sapiens (man)
Date: 02-Apr-1982 #text_change 09-Jul-2004
Accession: A90933; A90249; A20150
Blison, J.; Buxbaum, J.; Acod, L.
Al. 11-18, 1981
Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
Reference number: A90933; MUID:83157104; PMID:6299662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: DNA

Mesidues: 1-327 <ELL>

:Cross-references: UNIPROT:P01861

:Noce: the sequence was determined from the germline gene

:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

:Ochem. J. 117, 1347, 1970

:Title: Human immunoglobulin sublclasses. Partial amino acid sequence of 

Reference number: A90249; MUID:70207560; PMID:4192699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                         PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                     Gene: GBB:IGHG4
Cross-references: GDB:119340; OMIM:147130
Map position: 14432.33-14432.33
Introns: 99/1; 111/1; 221/1
Complex: An immunoglobulin heterotetramer subunit consists of two id in disulfide bonds. In some cases, such as IgA and IgM, the subunits Superfamily: immunoglobulin C region; immunoglobulin homology Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin 20-85/Domain: immunoglobulin homology <IMI>
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;Species: Oryctolagus cuniculus (domestic rabbit)
                                                                                                                                                                                                                                      gamma-4 chain C region - human Species: Homo sapiens (man)'
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Residues: 1-30;81-326 <PIN>
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Matches
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A; Molecule type: protein
A; Residues: 129-131,155-172, 'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q',;
A; Residues: 129-131,155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q',;
A; Note: this has the els allotypic marker, 185-Ala
C; Complex: An immunoglobulin heteroteramer subunit consists of two identical light (kapp
hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into lan
C; Superfamily: immunoglobulin C region; immunoglobulin homology
K; Reywords: duplication; alycoprotein; heterotetramer; immunoglobulin
F; 20-82/Domain: immunoglobulin homology < IM2>
F; 130-199/Domain: immunoglobulin homology < IM3>
F; 130-199/Domain: immunoglobulin homology < IM3>
F; 131-199/Domain: immunoglobulin homology < IM3-
F; 131-199/Domain: immunoglobulin homology < IM3-
F; 131-199/Domain: im
C,Date: 24-Apr-1984 #sequence revision 15-Nov-1984 #text change 09-Jul-2004
C,Accession: A91749; A90290; A9328; A90245; A94416; A02161
K;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot)
A;Reference number: A91749; MUID:84030930; PMID:6313520
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-323 < BER>
A; Cross-references: UNIPROT.P01870
A; Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
R; Pratt, D.M.; Mole, L.E.
Biochem. J 151, 337-349, 1975
A; Title: Sequence studies on the constant region of the FG sections of rabbit immunoglobu
A; Reference number: A90290; MUID:76135469; PMID:1243651
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A,Residues: 1-47, E',49-71, PV',72-128 <PRA>
R,Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A,Title: Heavy chain genes of rabbit 1gG; isolation of a cDNA encoding gamma heavy chain A,Reference number: A93928; MUID:83299917; PMID:6193512
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A; Residues: 88-103, M', 105-143, E', 145-184, A', 186, 'E', 188-266 < MAR>
A; Cross-references: GB:M16426; NID:g165111; PIDN:AA31289.1; PID:g165112
A; Notes: this sequence has the dil allotypic marker, 104-Met, and the e15 allotypic marke:
R; Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
A; Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin
A; Reference number: A90245; MUID:70110015; PMID:5461106
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A;Residues: 132-143,'E',145-161 <FRU>
KHill, R.L., Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,
A;Reference number: A94416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 KCKVSNKALPAPIEKTISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAV 164
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Iggamma-2 chain C region - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #seguence revision 07-May-1981 #text_change 09-Jul-2004
C;Accession: A94553; A90352; A90384; A90385; A02151
R;Trischmann, T.M.
R;Trischmann, T.M.
A;Molecule to the Atlas, April 1975
A;Accession: A94553
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: Ja - ATIS
A;Molecul
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[Species: Sus scrofa domestica (domestic pig)

[C)Species: Sus scrofa domestica (domestic pig)

[C)Accession: 147162

[R)Kacskovics, I.; Sun, J.; Butler, J.E.

R)Kacskovics, I.; Sun, J.; Butler, J.E.

A)Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a shacession: 147162

A)Accession: 147162

A)Acces
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                                                                                       PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVGS 188
                                                                                                                                169 GQTREPQVYTLPPPTEELSRSKVTLTCLVTGFYPPDIDVEWQRNGQPEPEGNXRTTPPQQ 228
TAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTRE 224
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                          189 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSPGK 232
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69.0%; Pred. No. 4.1e-58;
iive 32; Mismatches 35;
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Best Local Similarity 69.0
Matches 158; Conservative
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A, Molecule type: protein
A, Residues: 4-68 <BIR>
R, Turner, K.J.; Cebra, J.J.
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Riacskovics, 1; Sun, J.; Butler, J.E.
J. Immunol. 153, 356-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Attle: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Atatus: I47150
A;Atatus: preliminary, translated from GB/EMBL/DDBJ
A;Atatus: preliminary
A;Residues: 1-328 «KAC>
A;Residues: 1-328 «KAC>
A;Coss-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C;Genetics: A;Coss-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C;Genetics: A;Coss-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C;Genetics: Immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM'>
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R;Kacskovics, I.; Sun, J.; Butler, J.E.
R;Kacskovics, I.; Sun, J.; Butler, J.E.
A,Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A,Reference number: 147158; MUID:95015845; PMID:7930579
A;Accession: 147159
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                          gamma 2b chain constant region - pig (fragment)
Species: Sus scrofa domestica (domestic pig)
jate: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
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A;Abdecule type: mRNA
A;Residues: 1-128 < KAC>
A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
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F;133-202/Domain: immunoglobulin homology <IVM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.9%; Score 868.5; DB 2; Length 70.1%; Pred. No. 2.8e-58; ive 32; Mismatches 32; Indels
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Local Similarity 70.1%; Pred. No. 2.8e-58;
tes 157; Conservative 32; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity 70.1
157; Conservative
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Matches 157,
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36; DB 2;

Length 328;

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223

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70 HNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 EPQVYTLPPPAEELSRSKVTLTCLVIGFYPPDIHVEWKSNGQPEPENTYRTTPPQQDVDG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 HTAETRPKEEQFNSTYRVVSVLPIQEQDWLKGKEFKCKVNNVDLPAPITRTISKAIGQSR
A,Molecule type: mRNA
Kresiduss: 1.328 «KAC>
A;Cross.references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRIPEVICVVVDVSHEDPEVKFNWYVDGVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                          A;Gene: IgGl
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <1PM>
                                                                                                                                                                                                                                                                                                         67.3%; Score 847.5; DB 2 69.3%; Pred. No. 1.1e-56; tive 30; Mismatches 36
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Best Local Similarity 69.3*
Matches 156; Conservative
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Residues: 227-311 cTR2>
Oliveira, B.; Lam, M.E.
Oliveira, 10, 26-31, 1971
Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
Title: Interchain disulfide bonds
Tochents: annotation; disulfide bonds
Note: Cys-16; Gys-107, and Cys-110 form inter-heavy chain bond
Note: Cys-16; Gys-107, and Cys-110 form inter-heavy chain bonds
Note: Cys-16; Gys-107, and Cys-110 form inter-heavy chain bonds
Note: Cys-16; Gys-107, and Cys-110 form inter-heavy chain bonds
Note: Cys-16; Gys-107, and Cys-110 form inter-heavy chain bonds
Note: Cys-16; Gys-107, and Cys-110 form inter-heavy chain bonds
Note: Cys-16; Gys-107, and Cys-110 form inter-heavy chain bond
Note: Cys-16; Gys-107, and Cys-110 form inter-heavy chain bond
Note: Cys-107, and Cys-110 form inter-heavy chain bond
Superfamily: immunoglobulin heterotetramer subunit consists of two identical light (kap
List-204/Domain: immunoglobulin homology clM2>
24-310/Domain: immunoglobulin homology clM3>
28-79/Disulfide bonds: #status experimental
178/Binding site: carbohydrate (Asn) (covalent) #status experimental
24-8308/Disulfide bonds: #status experimental
ochemistry 10, 9-17, 1971
Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Ami
Reference number: A90359; MUID:71058486; PMID:5538616
                                                                                                                                                          Molecule type: protein
Residues: 69-133;312-329 <TUR>
Tracey, D.E.; Cebra, J.J.
cochemistry 13, 4796-4803, 1974
Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
Reference number: A90384; MUID:75036072; PMID:4429665
                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: protein
Residues: 134-226 «TRA»
Trischmann, T.M.; Cebra, J.J.
ochemistry 13, 4804-4811, 1974
Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
Reference number: A90385; MUID:75036073; PMID:4609467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 ISKTKGAPRMPDVYTLPPSRDELSKSKVSVTCLIINPFPADIHVEWASNRVPVSEKEYKN 276
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68.1%; Score 858; DB 1; Length 329;
Best Local Similarity 67.4%; Pred. No. 1.7e-57;
Matches 157; Conservative 28; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                           Accession: A90384
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Accession: 147158 | Racskovics, I.; Sun, U.; Butler, U.E. | Immunol. 153, 3565-3573, 199 | Title: Five putative subclasses of swine 1gG identified from the cDNA sequences | Reference number: 147158; MUID:95015845; PMID:7930579

Status: preliminary; translated from GB/EMBL/DDBJ

Accession:

gamma 1 chain constant region - pig (fragment)
;Species: Sus scrofa domestica (domestic pig)
;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

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284 TFFLYSKLAVDKARWDHGDKFECAVMHEALHNHYTQKSISKTQGK 328
                                                                                                                               Search completed: October 27, 2004, 17:04:51
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Q6gmx6 homo sapien
Aah64496 homo sapien
Aah64496 homo sapien
Bac85173 homo sapien
C6jp14 homo sapien
Q6jp14 homo sapien
Q7z75 homo sapien
Q7z75 homo sapien
Q5p14 homo sapien
Q5p14 homo sapien
Q5p14 homo sapien
Aah14258 homo sapien
Aah14258 homo sapien
Aah12514 homo sapien
Aah1847 homo sapien
Aah1847 homo sapien
Aah1848 homo sapien
Bac85318 homo sapien
Bac8518 homo sapien
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1 EPKSCDKTHICPPCPAFELL.......MHEALHNHYQQRSLSLSPGK 232
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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BAC85237
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AAH19337
Q6GMX6
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BAC85173
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1: uniprot_sprot:*
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ALIGNMENTS

STANDARD; PRT; 330 AA. 66 (Rel. 01, Created) 76 (Rel. 45, Last sequence update) 77 (Rel. 45, Last annotation update) 78 (Rel. 45, Last annotation update) 79 (Rel. 45, Last annotation update) 70 (Rel. 45, Last annotation update) 80 (Rel. 45, Last annotation update) 81 (Rel. 45, Last annotation update) 82 (Rel. 46, Last annotation update) 82 (Rel. 46, Last annotation update) 83 (MAELORA PROMEN E) 84 (Rel. 10:4071-4079(1982). 85 (Res. 10:4071-4079(1982). 86 (Rel. 47) 87 (Rel. 47) 88 (Rel. 47) 89 (Rel.	CI HUMAN CI HUMAN 1.015.19 1.001-1986 1.007-2014 dag gamma-104 dame=1GHG1; one sapiens EDUINE=82274; EDUINE=82274; EDUINE=82274; EDUINE=82274; EDUINE=82274; EDUINE=82274; EDUINE=1064 ED
	RESCULT 1 2GC1 HUMAN ACC P1087.7 1D GC1 HUMAN DT 21-UUL-19 DT 21-UUL-19 DT 21-UUL-19 DT 21-UUL-19 DT 21-UUL-19 DT 01-OCT-20 DT 01-OCT-20 DOWN Name-IGHG OC ENEXPYCH OR EN INTERPORT RA MEDINE-3 RA BILISON U RA MEDLINE-3 RA SCHMICH W RE SEQUENCE RA MEDLINE-8 RA SCHMICH W RE SEQUENCE RA SCHMICH W RE SEQUENCE RA MEDLINE-8 RA SCHMICH W RE SEQUENCE RE MEDLINE-8 RE SEQUENCE RE MEDLINE-8 RE SECUENCE RE RE SECUENCE RE RE RESECUENCE RE RE RESECUENCE RESECUE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-A resolution.";

Biochemistry 20:236-12370(1981).

I Biochemistry 20:236-12370(1981).

I MINCELLANBOUS: Nie has the GIM(17) allotypic marker, 97-K, and the GIM(1) marker and the GIM (non-1) markers.

I MINCELLANBOUS: Nie also differs in the amidation states of 35, 116, 198, 269 and 272.

I MINCELLANBOUS: EU also differs in the amidation states of residues:

I MINCELLANBOUS: EU also differs in the amidation states of residues 268-272.
                                                                                                                                           DISULPIDE BONDS.
MEDLINE=77070267; PubMed=1002129;
MEDLINE=77070267; PubMed=1002129;
MEDLINE=77070267; PubMed=1002129;
Melber L., Schwarz J., Reichel W., Hilschmann N.;
Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- MISCELLANEOUS: KOL also differs in the amidation states of residues 198, 267 and 272.
Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds ";
Biochemistry 9:3188-3196 (1970).
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PROSITE; PSG0835; IG_LIKE; 3.
PROSITE; PSG0290; IG MHC; 2.
3D-structure; Direct_protein sequencing; Glycoprotein;
Immunoglobulin C region; Immunoglobulin domain.
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PDB; 1AJ7; X-ray; H=1-101.

PDB; 1D5B; X-ray; H=1-101.

PDB; 1D5B; X-ray; H=1-101.

PDB; 1D5C; X-ray; H=1-101.

PDB; 1DK2; X-ray; A/B=106-329.

PDB; 1E4K; X-ray; A/B=106-329.

PDB; 1FC2; X-ray; A/B=106-329.

PDB; 1FC2; X-ray; A/B=106-329.

PDB; 1FC2; X-ray; A/B=106-329.

PDB; 1HZ; X-ray; A/B=107-330.

PDB; 1HZ; X-ray; B/D=1-103.

PDB; 1HZ; X-ray; A/B=107-330.

PDB; 1IX; X-ray; A/B=107-330.

PDB; 1IX; X-ray; A/B=107-330.

PDB; 1IX; X-ray; A/B=107-330.

PDB; 1OQX; X-ray; A/B=107-330.

PDB; 1OQX; X-ray; A/B=107-330.

PDB; 1QX; X-ray; A/B=107-330.

PDB; 2RCS; X-ray; A/B=107-330.

PDB; 1DQC; X-ray; A/B=107-330.

PDB; X-ray; A/B=107-330.

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MEDLINE=81208100; PubMed=7236608;
Deisenhofer J.;
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PIR; A93433; GHHU.
PDB; 1AJ7; X-ray; H=1-103.
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EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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K -> R (in GlM(3) marker).
/FIG=VAR 002886.
D -> E (in GlM(non-1) marker).
/FIId=VAR 003887.
L -> M (in GlM(non-1) marker).
/FIId=VAR_003888.
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97.2%; Score 1225; DB 1;
Best Local Similarity 97.0%; Pred. No. 1.8e-89;
Matches 225; Conservative 3; Mismatches 4;
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Matches 225; Conservative
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                                                                                                                           278
                                                                                       ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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               NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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TISSUE-Bermoid tumor;

Ota T., Nakagawa S., Senob A., Mizuguchi H., Inagaki H., Suzuki Y.,

Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,

Sugiyama T., Irie R., Otsuki T., Saro H., Nishikawa T., Sugiyama A.,

Kawakami B., Nagai K., Isogai T., Sugano S.;

"NEDO human cDNA sequencing project.";

"NEDO human cDNA sequencing project.";

"Submitted (UGL-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AKI29809; BAC68237.1;

EMBL; AKI29809; BAC68237.1;

EMBL; AKI29809; BAC68237.1;
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BAC86226 PRELIMINARY; PRT; 447 AA.

02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ43645 fis, clone SYNOV3000302, highly similar to Ig gamma-chain c region.

Hown sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                 232
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                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primata; Catarrhini; Hominidae; Homo.
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02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ26298 fis, clone DMC07404, highly similar to Ig
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Best Local Similarity 97.0
Matches 225; Conservative
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NCBI_TaxID=9606;

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REC TISSUB-PTIMINARY B-COLLS;

K NEDLINE=22388257; PubMed=12477932;

R Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B. A., Buetow K.H., Schaefer C.P., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

RA Expleton M., Moore T., Max S.L., Wang J., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M., Soares M.B., Rochiyuki S., Carninci P., Frange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Hidron D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

Rabes S.A., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Hidring M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Richards R.R., Touchman J.W., Green E.D., Dickson M.C.,

Radesiley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Radesiley M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

Richards S.J., Marra M.A.,

Rocheration and initial analysis of more than 15,000 full-length human
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[1]
SEQUENCE FROM N.A.
TESTIDE-SYNOVial membrane tissue;
Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
Fukuzumi Y., Fuljinorii Y., Koninyama M., Sugiyama T., Irie R.,
Kawai-Hio Y., Saito K., Makanatsu A., Ishii S., Yamanoto J., Isono Y.,
Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashira H.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
Murakawa K., Kanehori K., Takahashi-Fulii A., Oshima A., Sugiyama A.,
Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isogai T.;
"NEDO human cDNA sequencing project.";
submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AK125633; BAC86226.1;
SEQUENCE 447 AA; 49289 MW; F28884C17E89E8EF CRC64;
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. 2.5e-89;
3; Mismatches 4;
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XR TISSUE-Frimary B-Cells;

XR Tausberg R.D., Collins F.S., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wann J., Hashe F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wahn J., Hong L.,

Altschul S.F., Jordan H., France A., Rubin G.M., Hong L.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A platchenko L., Marusina T.B., Toshiyuki S., Carninol B.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Youchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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                                                                                                                                                                                                     97.2%; Score 1225; DB 2; Length 464; 97.0%; Pred. No. 2.7e-89;
                                                                                                                                                                                                                                                4; Indels
                                                       Strausberg R.; Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC019337; AAH19337.1; -. Hypothetical protein. SEQUENCE 464 AA; 50891 MW; 2F80673E74E2A485 CRC64;
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073766; AAH73766.1; -.
InterPro; IPR003599; Ig.
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Last annotation update)
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c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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3; Mismatches
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                                                                                                                                                                                                                                                   Conservative
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                                        TISSUE=Primary B-Cells;
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TISSUE=Primary B-Cells;
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es 225; Conserv
                        FROM N.A.
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[2]
SEQUENCE 1
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TISSUB-PETIPHERAL Nervous System;

TISSUB-PETIPHERAL Nervous System;

MEDINE-2238825; PubMed=1247921;

A Straubberg R.L.; Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Rischul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhar N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A.M. Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M. Gay L.J., Hulyk S.W.,

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Richards S., Worley W.C., Shevchenko Y., Boulfard G.G.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1225; DB 2;
Pred. No. 2.7e-89;
3; Mismatches 4;
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UR INTERPO; IPR003597; Ig-cl.

DR INTERPO; IPR003597; Ig-cl.

DR INTERPO; IPR003506; Ig_WHC.

DR Pfam; PF00764; Cl-set; 3.

DR Pfam; PF00764; ig, 4.

DR SMART; SM00407; Ig; 4.

R PR05ITE; PS00835; Ig_LIKE; 4.

R PR05ITE; PS00290; IG_MHC; UNKNOWN_2.

HYPOCHETICAL PEOCHER.
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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TISSUE-Spleen;

MEDINE-2598257; PubMed=12477932;

Attausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Attachul S.F., Zeeberg B., Buetow K.H., Schaefer C.R., Shuler G.D.,

Attachul S.F., Zeeberg B., Buetow K.H., Schaefer C.R., Bhar N.K.,

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Bornstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevothenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevothenko Y., Bouffard G.G.,

Rodriguez A.C., Girmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Unes S.J., Marra M.A.;
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AAH64496;
AAH6496;
A. (TEVBLrel. 27, Created)
02-MAR-2004 (TEVBLrel. 27, Last sequence update)
02-MAR-2004 (TEVBLrel. 27, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE FROM N.A.

TISSUE=beripheral Nervous System;
Strausberg R.;
Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC072419; AAH72419.1;
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR0030596; Ig.
InterPro; IPR0040596; Ig.
SMART; SM00409; IG; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.2%; Score 1225; DB 2; 97.0%; Pred. No. 2.7e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 2.7e
3; Mismatches
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5; Conservative
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180
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"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
Kawakami B., Nagai K., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (JUL-2003) to PEMBL/GenBank/DDBJ databases.
EMBL; AKI29512; BAC85173.1;
SEQUENCE 467 AA; 50782 MW; 632AEA2D6CD248F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVLDSDGSFFLYSKLIYUDKSRWQQGNVFSCSVWHEALHNHYIQKSLSLSPGK 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primata, Catarrhini, Hominidae, Homo.
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                                                                                         SECUENCE FROM N.A.
TISSUE-spleen;
Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; 8D064499; AAH64496.1;
Fypothetical protein.
SEQUENCE 466 AA; 51078 MW; 13F032EDAC9DBC22 CRC64:
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02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ26001 fis, clone DMC07585, highly similar to
                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                   97.2%; Score 1225; DB 2;
97.0%; Pred. No. 2.7e-89;
tive 3; Mismatches 4;
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97.0%; Pred. No. 2.7e-89;
iive 3; Mismatches 4;
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Best Local Similarity 97.09
Matches 225; Conservative
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Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Lausner R.D., Collins F.S., Wagner L., Shaefer C.F., Schuler G.D., Altschul S.F., Zeeberg B., Buertow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Latchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toobhyuki S., Carnhori P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernan K.J., Malek J.A., Gunzarene P.H., And Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Avilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W., Whiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Schnerch A., Jones S.J., Marra M.A.,
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  232
                             PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC037361, AAH37361.1; -.
Hypothetical protein.
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                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Pred. No. 2.7e-89;
3; Mismatches 4;
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Best Local Similarity 97.0%;
Matches 225; Conservative
                                                                                                                                                                                                                        02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, Hypothetical protein. Homo sapiens (Human).
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                                                                                                                                                                             PRELIMINARY;
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TISSUE=Spleen;
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                                                416
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                                                                  02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ26006 fis, clone DMC08725, highly similar to Ig gamma-1 chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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02-MXR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ27334 fis, clone TMS09201, highly similar to Ig gamma-1 chain
C region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Sugiyama A.,
                                                                                                                                                                                                                                                                                                             SEQUENCE: T. Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y., TISSUE-Dermoid tumor;

Ota T., Nakagawa S., Senoh A., Mizuno B., Kawamura M., Hate H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Izie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B., Nagai K., Isogai T., Sugano S.;

NEDO human cDNA sequencing project.";

Submitted (JUL-2003) to the BMEL/GenBank/DDBJ databases.

SHOBL; AK129517; BAC85175.1; -- TICS19D86AE3D44B CRC64;
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ENkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                               Euteleostomi;
Homo.
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Nakagawa K., Mizuno S., Motinaga M., Kawamura M., Sugiyama T.,
Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T.,
Sugano S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
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Pred. No. 2.7e-89;
3; Mismatches 4; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 468;
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AK130844; BAC85444.1;
EMBL; AK1308444; BAC85444.1; 9280ACAD6817FC20 CRC64;
                                                                                                                                                                                  Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Primata, Catarrhini, Hominidae, NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.2%; Score 1225; DB 2;
97.0%; Pred. No. 2.7e-89;
iive 3; Mismatches 4;
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02-WAR-2004 (TrEMBLrel. 27, Last seq
02-WAR-2004 (TrEMBLrel. 27, Last ann
                                               Created)
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ilarity 97.0%;
Conservative
                                             (TrEMBLrel. 27,
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les 225; Conservative
PRELIMINARY;
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Homo sapiens (Human)
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TISSUE=Thymus;
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                                               02-MAR-2004
02-MAR-2004
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Best Local Simi
Matches 225;
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BAC85444;
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BAC85175
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MEDLINE-22388257; PubMed=12477912;

MEDLINE-22388257; PubMed=12477912;

MIDLINE-22388257; PubMed=12477912;

MIDLINE-22388257; PubMed=12477912;

MIDLINE-22388257; PubMed=12477912;

MIDLINE-22388257; PubMed=12477912;

MIDLINE-22388257; PubMed=12477912;

MIDLINE-22388257; MIDLINE-238826;

MIDLINE-2388257; MIDLINE-238826;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Strauberg Rank-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC051328, AAH51328.1; -
InterPro; IPR003597, Ig_cl.
InterPro; IPR003596, Ig_W.
InterPro; IPR003596, Ig_W.
Pfam; PF0764; Cl-set; 3.
Pfam; PF0764; ig; 1.
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PROSITE; PS00290; IG WHC; UNKNOWN 2.
SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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TISSUE-Spleen;
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MEDINE=2238825; PubMed=12477932;
MEDINE=2238825; PubMed=12477932;
Strausberg R.L., Felngold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Felngold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Bronstein M.J., Usdin T.B., Robaldo M.F., Casavant T.L., Scheetz T.E.,
Bronstein M.J., Usdin T.B., Toshiyuki S., Carninol P., Prange C.,
A Raha S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Miting M., Madan A., Young A.C., Shevcheko Y., Boutfard G.G.,
Miting M., Madan J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz D., Myers R.M., Butterfield Y.S.,
M. Krzywinski M.I., Skaiska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                             238 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF
                                                                                                                                          121 ISKAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
                                                                                                                   61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                        1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Indels
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO18747; AAH18747.1;
InterPro; IPR003599; Ig. 11ke.
InterPro; IPR003597; Ig. 21.
InterPro; IPR003597; Ig. 21.
InterPro; IPR003596; Ig. MHC.
InterPro; IPR003596; Ig. MHC.
Pfam; PF00647; 11-set; 3.
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05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
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4;
Mismatches
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SMARY; SMO0409, 1G; 2.
SMARY; SMO0407, 1Gc1; 3.
SMARY; SMO0406, IGV, 1.
PROSTIE; PS50835; IG LIKE; 4.
PROSTIE; PS00290; IG_MHC; UNKNOWN_2.
3.
225; Conservative
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TISSUE=Primary B-Cells;
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Homo sapiens (Human).
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Search completed: October 27, 2004, 17:03:56
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Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Appking R.F., Jordan H., Moor T., Max S.I., Wang J., Hsieh F.,
Appking R.F., Jordan H., Moor T., Max S.I., Wang J., Hsieh F.,
Appleton M., Soars M.B., Bonaldo M.F., Carainci P., Frange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carainci P., Frange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carainci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan R.J., Makek J.A., Guazatne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Schmutz J., Msrra M.J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
The Moore S.J., Marra M.A.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                Length 470;
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Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC053984; AAH53984.1;
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig c1.
InterPro; IPR003596; Ig MHC.
InterPro; IPR003596; Ig V.
Pfam; PF007654; C1-set; 3.
                           7B49556A11FD7D99 CRC64;
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Last annotation update)
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                                                                             cch 97.2%; Score 1225; DB 2; al Similarity 97.0%; Pred. No. 2.7e-89; 225; Conservative 3; Mismatches 4;
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MEDLINE=22388257; PubMed=12477932;
   1 protein.
470 AA; 51715 MW;
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   Hypothetical
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02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last sentocation update)
CDNA FL286276 fis, clone DMC06522, highly similar to 1g gamma-1 chain
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Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
Itata H., Nakagawa S., Mizuno S., Morinaga M., Kawamura M.,
Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
Rawakami B., Nagai K., Isogai T., Sugano S.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 470 AA; 51090 MW; 460F4717D4528A16 CRC64;
                                                    Hypothetical protein.
SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;
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al Similarity 97.0%; Pred. No. 2.7e-89;
225; Conservative 3; Mismatches 4;
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3, Mismatches
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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Homo sapiens (Human)
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Copyright (c) 1993 - 2004 Compugen Ltd.	using sw model	2004, 16:31:18 ; {;	9-3
Copyright	protein - protein search, using sw model	October 27,	US-10-000-439-3
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1260 1 BPKSCDKTHTCPPCPAPELL......MHEALHNHYQQRSLSLSPGK 232 tle: rfect score: squence:

2002273 seqs, 358729299 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 oring table: sarched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

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SUMMARIES

Description	Human Ig	Aao19664 Human IgG	668 GE2 fu	5232 Human	Aab28690 Human IgG	97 Human	15 Human	5347 Human	5272 Human I	1 Herpes	7512	9463 Human	3647 pCXFc.	39055 Plasmi	47 Binding	Adg74307 Fibroblas	74 Human	1490 Human		154 Protei	273 Huma	_	Aab47590 Fusion pr	1806 Human i	Aab04071 Zcytor 10
ID	AA019665	AA019664	AA019668	AAW26232	AAB28690	AAB80897	AAY72915	AAE15347	AAE26272	ADJ65991	ADJ57512	ABB09463	ABJ38647	ADA89055	ADD25647	ADG74307	AAE26274	ABB81490	AAE35214	AAY24154	AAE26273	ADJ52120	AAB47590	AAR91806	AAB04071
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	Aae21960 Human dea	Abb81641 Human IgG	Abb05736 Human imm	Abp71856 Human IgG	Aae32915 Human imm	Aae32627 Human imm	Abr82103 Human DR6			Aao30893 Human imm	Adf11389 Anti-OPGL	Ade97351 Human IgG	Adf83605 Cytokine	Adf75001 Human Ig	Adm41537 Anti-inte	Adm68911 Human IgG	Adn36570 Chemokine	Adn97485 Artificia	Aay91106 Human TR-
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AAM47856	AAE21960	ABB81641	ABB05736	ABP71856.	AAE32915	AAE32627	ABR82103	AA031102	ABR55836	AA030893	ADF11389	ADE97351	ADF83605	ADF75001	ADM41537	ADM68911	ADN36570	ADN97485	AAY91106
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26	27	28	56	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

Human IgG1 heavy chain constant region hinge-CH2-CH3 portion. AAO19665 standard; protein; 232 AA (first entry) 28-MAR-2003 AA019665; AA019665

Human, IgG1, immunoglobulin G; immunotherapy; immune disease; Forepsilon receptor; autoimmune disease; constrant region, heavy chain; antiasthmatic; antiallergic; antiinflammatory; dermatological; antiarthritic; antirheumatic; antidiabetic; neuroprotective; hinge-CH2-CH3 region

Homo sapiens,

WO200288317-A2. 07-NOV-2002. 01-MAY-2002; 2002WO-US013527.

01-MAY-2001; 2001US-00847208. 24-OCT-2001; 2001US-0000439.

(REGC) UNIV CALIFORNIA.

Saxon A, Zhang K, Zhu D; WPI; 2003-103456/09. New fusion molecules comprising polypeptide sequences that bind to IgG inhibitory receptor and native IgE receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases.

Claim 19; Fig 3; 116pp; English.

The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (TIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor specific binding directly or indirectly to a native IgE receptor (FeepsilonR). Also provided are nucleotide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for

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treating an IgE-mediated biological response, preferably an IgE-mediated hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-I diabetes mellitus, or multiple sclerosis, and for preventing of, or swaptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is the human IgG1 heavy chain constant region hinge-CH2-CH3 portion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fusion molecules comprising polypeptide sequences that bind to Ig(lbitory receptor and native IgE receptor, useful for treating IgE-lated hypersensitivity reactions, e.g. asthma or allergies, or
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                                                                                                                                                                                            Score 1260; DB 6;
Pred. No. 2.8e-91;
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24-OCT-2001; 2001US-00000439.
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                                                                                                                                                                                                               Similarity
                                                                                                                                                             Sequence 232 AA;
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inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (TIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor (Fcepsilons). Also provided are unclectide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for treating an IgE-mediated biological response, preferably an IgE-mediated bringing and a sathma, allergic rhintis, a topic dermatitis, severe food allergies, chronic urticaria, angloedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-I diabetes mellituus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is the human IgGI
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GE2;
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                                                                                                                                                                                                                                                                                               100.0%; Score 1260; DB 6; Length 330; 100.0%; Pred. No. 4.2e-91;
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24-OCT-2001; 2001US-00000439.
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Unidentified.
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New fusion molecules comprising polypeptide sequences that bind to

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inhibitory receptor and native IgE receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or
                                                                                                        autoimmune diseases.
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WPI; 1997-402624/37. N-PSDB; AAT80158.

Claim 35; Fig 7; 116pp; English.

The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor (FeepsilonR). Also provided are nucleotide sequences encoding such fusion protein. The fusion molecules and compositions are useful for treating an IgE-mediated biological response, preferably an IgE-mediated hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angiedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-I diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is a gammahinge-CHgamma2-CHgamma3-(Gly4Ser)3-CHepsilon2-CHepsilon3-CHepsilon3 fusion protein (designated GE2) of the invention

Sequence 569 AA;

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120
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100.0%; Score 1260; DB 6; Length 569; larity 100.0%; Pred. No. 8.1e-91; Conservative 0; Mismatches 0; Indels 0;
                                 Best Local Similarity
Matches 232; Conser
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      Query Match
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AAW26232 standard; protein; 232 AA (first entry) 16-MAR-1998 AAW26232;

Fusion protein; hydrophilic spacer; recombinant; express: carboxypeptidase; IgG1; immunoglobulin; hinge region; Fc Fusion protein; hydrophilic

Human IgG1 hinge/Fc region.

Homo sapiens

WO9728272-A1. 07-AUG-1997. 31-JAN-1997;

96US-00595043. 31-JAN-1996;

(TECH-) TECHNOLOGENE INC

Sgarlato GD;

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A novel recombinant vector has been developed which comprises a nucleotide sequence encoding a fusion protein. The fusion protein comprises three domains joined together in order, from N-terminus to terminus, of a first domain comprising a protein of interest, a second domain comprising anydrophilic spacer and an affinity domain, each the hingey for region of human IgG1, used in example 3 of the present the hingey for region of human IgG1, used in example 3 of the present invention. The recombinant vector is used for the production of authentic recombinant proteins of interest. The method of the invention is useful for the expression of fusion proteins capable of isolation by affinity chromatography in pro- or eukaryotic cells. This method allows for the efficient cleavage and generation of authentic proteins of interest that do not contain extraneous (i.e. non-naturally occurring) amino acids
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                                                                                        Recombinant protein expression system for fusion protein production - useful for high quantity production of authentic recombinant proteins.
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                                                                                                                                                                         Example 3; Page 133-134; 194pp; English
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Matches 225; Conservative
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Human, AGP-1; type II transmembrane protein; cytostatic; antiviral; antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV; human immunodeficiency virus; apoptosis; proliferative disorder; cancer; hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder; transplant rejection; cardiovascular disease; arteriosclerosis; Human IgGgammal hinge, CH2 and CH3 regions.

(first entry)

14-FEB-2001

Homo sapiens.

26-OCT-2000.

24-MAR-2000; 2000WO-US008004

16-APR-1999;

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of lytic bone disease or multiple myeloma. Also the method can be used the preventing metastasis of cancer to bone or osteosclerotic bone metastasis. The method comprises administering an OPG (osteoprotegrin) polypeptide or OPG fusion protein. The OPG proteins (see AAB80899) can inhibit formation of osteoclasts (and thus bone resorption) by blocking differentiation from monocytes/macrophage precursors. The present sequence is the hinge, CH2 and CH3 regions of human IgGgammal. This sequence can be used to generate fusion proteins of OPG and immunoglobulin, for use in the present invention. The generated fusion proteins can exhibit increased circulating half-lives and slower
                                                                           Preventing or treating lytic bone diseases, particularly associated with cancer or metastasis, by administering an osteoprotegrin polypeptide.
                                                                                                                                                      The present invention relates to a method for the prevention or treatment
                                                                                                                         Disclosure; Fig 1; 87pp; English
                                             WPI; 2001-265936/27.
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                                                                                                                                                                                                                                                                                                                                                          Sequence 232 AA;
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                Dunstan CR;
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                                                                                                                                                              The present sequence was used in the production of AGP-1 fusion proteins. AGP-1 is a type II transmembrane protein. The fusion proteins comprise an PC immunoglobulin region fused to the N-terminal portion of the AGP-1 protein. The fusion proteins can be used to induce apoptosis in a tissue, and to treat proliferative disorders, immune disorders, or virally-induced disorders. The proliferative disorders include cancers, such as breast, prostate, lung or colon cancer. The viral infections include hepatitis, and acquired immunodeficiency syndrome (ALDS), and the immune disorders may be autoimmune disorders or transplant rejection. Cardiovascular diseases such as arteriosclerosis may also be treated. The AGP-1 containing fusion proteins have increased biological activity compared to the soluble AGP-1 proteins used in prior art therapies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusion protein of AGP-1 protein and an Fc region, used to treat proliferative disorders, immune disorders, and virally-induced disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.2%; Score 1225; DB 3; Length 232; 97.0%; Pred. No. 1.6e-88; ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lytic bone disease, multiple myeloma, immunoglobulin, osteosclerotic bone metastasis, OPG; osteoprotegrin, osteoclast formation inhibition, bone resorption inhibition.
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                                                                                                                                      English.
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                                                                                                                                      Claim 2; Fig 1; 93pp;
                                                            WPI; 2000-665240/64.
(AMGE-) AMGEN INC
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Matches
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therspy; bone loss; osteoporosis; Paget's disease; osteomy-litts;
hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;
osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;
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clearance times, thereby providing a more sustained activity
                                                                                                                        Length 232;
                                                                                                                                                                                   4; Indels
                                                                                                                     Score 1225; DB 4;
Pred. No. 1.6e-88;
3; Mismatches 4;
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                                                                                                                     Query Match
Best Local Similarity 97.0%;
Matches 225; Conservative
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The patent discloses fusion protein comprising human osteoprotegerin (OPG) protein fused by linker to human 1gd1 Fc portion. OPG negatively regulates formation of osteoclasts in vitro and in vivo. It blocks the differentiation of osteoclasts from monocyte or mercephage precursors and the treatment of bone. The OPG-Fc fusion protein is administered for the treatment of bone loss resulting from osteoponis, Paget's disease, osteomyalitis, Mypercalcaemia, osteopenia associated with surgery or steroid administration, osteomecrosis, bone loss due to rheumatoid arthritis, periodontal bone loss, osteolytic metastasis and/or prosthetic lossening. The present sequence is partial human immunoglobulin G (Ig G) 1 protein comprising the hinge and heavy chain constant regions CH2 and CH3
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                                                                                                            for treating bone loss caused osteomyelitis.
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Pred. No. 1.6e-88;
3; Mismatches 4; Indels (
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                                                                                                            Osteoprotegerin-Fc protein fusions useful
by e.g. osteoporosis, Paget's disease and
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Mann MB;
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225; Conservative
Wooden SK,
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                                                      WPI; 2001-244572/25
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Dunstan CR,
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Best Local Si
Matches 225;
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The invention relates to a method for increasing and maintaining haematocrit in a mammal. The method comprises administering a hyperglycosylated analogue of erythropietin (Epo) in a pharmaceutical composition, less frequently than an equivalent molar amount of and at a lower molar amount than recombinant human Epo (rHuEpo) to obtain a comparable target hematocrit. Epo is a glycoprotein hormone necessary for the maturation of erythroid progenitor cells into erythrocytes. Human Epo analogue is useful for raising and maintaining haematocrit to a comparable target hematocrit in a mammal suffering from anaemia comparable target hematocrit in a mammal suffering from anaemia therapy comprising chemotherapeutic or anti-viral drugs or associated with a decline or loss of kidney function, myelosuppressive therapy comprising chemotherapeutic or anti-viral drugs or associated with excessive blood loss during surgical procedures, and in cancer condition. The present sequence is human immunoglobulin G (IgG) gamma 1 constant heavy chain (CH2, CH3) hinge region used to construct Epo
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                               Increasing and maintaining hematocrit in mammal suffering from anemia, comprising administering hyperglycosylated analog of erythropoietin less frequently and at lower molar amount of recombinant human erythropoietin.
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Pred. No. 1.6e-88;
3; Mismatches 4;
                                                                                                       Example 1, Fig 10; 95pp; English.
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Best Local Similarity 97.0%;
Matches 225; Conservative
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WPI; 2002-034433/04
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29-NOV-2000;
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cerebroprotective; cytostatic; vasotropic; antirheumatic; antiarthritic; antiarteriosclerotic; antiinflammatory; antibacterial; immunosuppressive; hypertensive; cardiant; coagulation Factor VII; human; immunoglobulin G1; IgG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention comprises a therapeutic agent for treating endotoxin induced disease, the therapeutic agent contains a fusion protein of the Herpes virus entry mediator (HYEM) protein and an immunoglobulin Fc domain. The therapeutic agent of the invention is useful for treating endotoxin induced disease, such as endotoxic shock. The present amino acid sequence represents a human protein which is claimed in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 BPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New therapeutic agent, useful for treating endotoxin induced disease, comprises fusion protein of Herpes virus entry mediator protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
endotoxin induced disease; fusion protein; mediator; HVEM; immunoglobulin Fc domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.2%; Score 1225; DB 7; 97.0%; Pred. No. 1.6e-88; iive 3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; SEQ ID NO 2; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADJ57512 standard; protein; 232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human 1gG1 Fc domain fragment.
                                                                                                                                                                                                                                    25-OCT-2001; 2001JP-00328430
                                                                                                                                                                                                                                                                                    25-OCT-2001; 2001JP-00328430
                                                                                                                                                                                                                                                                                                                                 KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                              (TAIS ) TAISHO PHARM CO (GENE-). GENE TECHNO SCI
therapeutic agent, endo
Herpes virus entry medi
endotoxic shock, human.
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-817833/77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADJ65998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin.
                                                                                                                                       JP2003128576-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specification.
                                                                                               Homo sapiens
                                                                                                                                                                                         08-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Simi
Matches 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asyloging and subject and the clearing an amylotugemic absolute studies as Alzheimer's disease and spongiform encephalopathy. Disorders treatable amyloid caused or characterised by deposits of TTR (eg. familial amyloid cardiomyopathy), PPP (eg. spongiform encephalopathy in cows and creuzfelde.Jacob disease (CJ) and Gerstmann.Straussler-Scheinker syndrome (GSS) in humans), IAPP (eg. insulinoma, adult onset diabetes), ANF (eg. isolated atrial amyloid, kappa or lambda light chain (eg. hereditary non-reuropathic systemic amyloidosis), Apo A-I (eg. hereditary non-reuropathic systemic amyloidosis), Apo A-I familial amyloidosis of Finnish type), Fibrinogen (eg. hereditary renal amyloidosis of Ennish type), Fibrinogen (eg. hereditary renal amyloidosis of Ennish type), Fibrinogen (eg. hereditary renal amyloidosis of myloidosis. The present sequence is human IgG1 heavy chain, used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                  The invention relates to a compound comprising an immunoglobulin (Ig) heavy chain constant region or its fragment that retains the ability to bind an PC receptor linked by a linker group or a direct bond to a peptide capable of binding an amyloidogenic protein. The invention is useful for clearing an amyloidogenic protein. The invention is transthyretin (TTR), prion protein (PrP), islet amyloid polygeptide (IAPP), atrial natriuretic factor (ANP), kappa light chain, lambda light chain, amyloid A, procalcitonin, cystatin C, beat2-microglobulin, ApoA-I, gelsolin, calcitonin, fibrinogen, Huntington, alpha-symuclein and lysozyme from a subject and for treating an amyloidogenic disorder such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18KAKVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                    Novel therapeutic agent useful for treating an amyloidogenic disorder, e.g. Alzheimer's disease, comprises an immunoglobulin heavy chain constant region linked to a peptide capable of binding amyloidogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 BPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   °;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.2%; Score 1225; DB 5; Length 232; 97.0%; Pred. No. 1.6e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
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                                                                                               Gosselin M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ą
                                                                                                                                                                                                                                                                                                             Example 8; Page 76; 79pp; English.
                                                                                          Joyal JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ65991 standard; protein; 232
  20-DEC-2000; 2000US-0257186P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                               (PRAE-) PRAECIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225; Conservative
                                                                                            Israel DI,
                                                                                                                                          WPI; 2002-636427/68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 232 AA;
                                                                                          Gefter ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-2004
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                                                                                                                                                                                                                                                             protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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Matches
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ADJ65991
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Gaps

Homo sapiens

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The invention relates to a compound (I) binding to tissue factor (TF). The compound (I) has the formula A-(LM)-C, where A is a FVIIa polypeptide, LM is an optional linker group, C comprises an polypeptide, LM is an optional linker group, C comprises an modification of factor domain, and (I) binds to TF. (I) inhibits TF-mediated activated factor VII (FVIIa) activity. (I) is useful as a medicament, and for the manufacture of a medicament for preventing or treating disease or disorder associated with pathophysiological TF activity. The disease or disorder associated with pathophysiological TF activity are deep venous thrombosis, arterial thrombosis, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transdermal coronary angioplastry (PTCA), stroke, cancer, tumor metastasis, angioplastry (PTCA), stroke, cancer, tumor metastasis, angioplastry (PTCA), stroke, cancer, tumor metastasis, and restenosis following angioplastry, acute and chronic indications such as inflammation, septic shock, septicemia, hypotension, adult respiratory distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC), pulmonary embolism, platelet deposition, myocardial infarction, or prophylactic treatment of mammals with atherosclerotic vessels at risk for thrombosis. The present sequence represents the Fc domain fragment of human immunoglobulin GI (19G1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New compound binding to tissue factor, useful for treating diseases such as anglogenesis, ischemia/reperfusion, and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Steenstrup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 16; SEQ ID NO 7; 61pp; English.
                                                                                                                                                                                                         09-JUL-2003; 2003WO-DK000481
                                                                                                                                                                                                                                                                                                                   12-JUL-2002; 2002DK-00001099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicolaisen EM,
                                                                                                                                                                                                                                                                                                                                                                                                                       (NOVO ) NOVO NORDISK
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WO2004006962-A2
                                                                                                          22-JAN-2004
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180
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                                                                                                                                                                                    NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
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                                                                             1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                             61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                        121 ISKAKVOPREPOVYTLPPSRDELTKNQVSLICLVKGFYPSDIAVEWESNGOPENNYKTTP
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                        PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                         ő
                                         4; Indels
Score 1225; DB 8;
Pred. No. 1.6e-88;
3; Mismatches 4;
    97.2%;
    Query Match
Best Local Similarity 97.0
Matches 225; Conservative
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120

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180 121

181

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ABJ38647 standard; protein; 235

RESULT 13 ABJ38647 (first entry)

26-JUN-2003

ABJ38647;

Human IgG Fc fragment amino acid sequence. ABB09463 standard; protein; 233 AA 01-JUL-2002 ABB09463;

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The invention relates to a transformant yeast that can present protein A or its fragment on its cell surface. The yeast can be used for detecting or isolating the Fc part of immunoglobulin (Ig)G. The yeast is useful for a stable supply of highly active catalytic antibody e.g. by screening novel functional molecules and in isolating Fc-carrying secretory to a combinatorial antibody library with an Fc-carrying antibody to a combinatorial antibody library with an Fc-carrying antibody component. The current sequence represents the human IgG Fc fragment
                                                                                                                                                                                                                                                                                                                                                                                                                        Transformant yeast for stable supply of highly active catalytic antibody, comprises the capability of expressing and presenting protein A or its fragment, particularly with the ZZ domain, on the cell surface.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
          Protein A; immunoglobin G; IgG; antibody; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1225; DB 5;
Pred. No. 1.6e-88;
3; Mismatches 4
                                                                                                                                           /note= "encoded by ACC"
                                                                                                           'note= "encoded by GAC"
                                                                  Location/Qualifiers
Misc-difference 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Fig 4; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                            Ueda M, Teranishi Y;
                                                                                                                                                                                                                                             04-JUL-2001; 2001WO-JP005788.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.2%;
                                                                                                                                                                                                                                                                           07-JUL-2000; 2000JP-00206689
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Best Local Similarity 97.0
Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-148174/19.
N-PSDB; ABL52834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 component. The curranino acid sequence
                                                                                                                           Misc-difference 169
                                                                                                                                                                                                                                                                                                             (GENC-) GENCOM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 233 AA;
                                                                                                                                                                          WO200204602-A1
                                             Homo sapiens
                                                                                                                                                                                                            17-JAN-2002
                                                                                                                                                                                                                                                                                                                                              Janaka A,
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ADA89055 standard; protein; 235 AA.

(first entry)

20-NOV-2003

pCXFc protein SEQ ID No 6.

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New molecules having the antigen-binding portion of antibodies that block activation of receptor protein tyrosine kinase, useful for treating or inhibiting skeletal dysplasias, craniosynostosis or cell proliferative
                      Cytostatic; osteopathic; cerebroprotective; dermatological; enzyme; antigen binding; receptor protein tyrosine kinase; skeletal dysplasia; constitutive activation; cranicosynostosis; cell proliferative disorder; achondroplasia; thanatophoric dysplasia; acanthosis nigricans dysplasia; hypochondroplasia; severe achondroplasia; transitional cell carcinoma; Muenke coronal calloarostosis; Crozin syndrome; acanthosis nigricans; tumour progression; osteosarcoma; chondrosarcoma; multiple mystoma; mammary carcinoma; fibroblast growth factor receptor 3; FGFR3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel molecule comprising the antigen binding
                                                                                                                                                                                                                                                                                                                                          Ξ,
                                                                                                                                                                                                                                                                                                                                          Rom
                                                                                                                                                                                                                                                                                                                                          Yayon A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 38; 103pp; English
                                                                                                                                                                                                                                       20-JUN-2002; 2002WO-IB003523.
                                                                                                                                                                                                                                                                   20-JUN-2001; 2001US-0299187P.
                                                                                                                                                                                                                                                                                                                                          Thomassen-Wolf E, Borges E,
                                                                                                                                                                                                                                                                                              (MORP-) MORPHOSYS AG. (PROC-) PROCHON BIOTECH LTD
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-167489/16.
                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABT40262.
                                                                                                                                                                                  WO2002102854-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 235 AA;
                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                             27-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders.
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portion of an isolated antibody, which has an increased affinity for a receptor protein tyrosine kinase and which blocks constitutive activation of the receptor protein tyrosine kinase. The methods and compositions of the invention are useful for treating or inhibiting a skeletal dysplasia or aniosynoatosis or a cell proliferative disorder. The skeletal dysplasia is achondroplasia, thanatophoric dysplasia, hypochondroplasia, severe achondroplasia with developmental delay or acanthosis ingricans dysplasia in the craniosynostosis of crouge disorder is Muenke coronal craniosynostosis or Crouzin syndreme with acanthosis ingricans. The cell proliferative disorder is tumour progression that is progression of transitional cell carcinoma, osteosarcoma, chondrosarcoma, multiple myeloma or mammary carcinoma. This sequence represents a protein derived from a pCXFC plasmid DNA vector relating to the protein tyrosine kinase inhibitor of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.2%; Score 1225; DB 6; Length 235; 97.0%; Pred. No. 1.6e-88; ive 3; Mismatches 4; Indels
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Les 225; Conservative
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Matches
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New antibodies which have specific binding affinity for a receptor protein tyrosine kinase (RPTK) and block constitutive activation of RPTK, useful for treating bone and cartilage disorders, or malignant cell
                                                                                  antigen binding, antibody, specific binding affinity, receptor protein tyrosine kinase; RPTK, receptor protein tyrosine kinase inhibitor; receptor protein tyrosine kinase inhibitor; fibroblast growth factor receptor; FGFR, osteopathic; cytostatic; ophthalmological, bone disorder; cartilage disorder; skeletal disorder; skeletal dysplasia; achondroplasia; thanatophoric dysplasia; hypochondroplasia; craniosynostosis disorder; thanatophoric disorder; malignant cell proliferative disease; cancer; tumour; vision disorder; non-neoplastic angiogenic pathologic condition.
                                                                 Plasmid pCXFc amino acid sequence SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                        20-JUN-2001; 2001US-0299187P.
                                                                                                                                                                                                                                                                                  20-JUN-2002; 2002WO-IL000495
                                                                                                                                                                                                                                                                                                                               (PROC-) PROCHON BIOTECH LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                              proliferative diseases.
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-175236/17; N-PSDB; ADA89054.
                                                                                                                                                                                                                                                                                                                                                     Yayon A, Rom E;
                                                                                                                                                                                                                                      WO2002102973-A2
                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                             27-DEC-2002.
                                                                                                                                                                                                     Synthetic.
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The present invention describes a molecule (I) comprising the antigen binding portion of an isolated antibody which has specific binding affibroblast growth factor receptor (FGFR), and which blocks constitutive a tibroblast growth factor receptor (FGFR), and which blocks constitutive comprising (I) as an active ingredient and a pharmaceutical carrier, comprising (I) as an active ingredient and a pharmaceutical carrier, comprising (I) as an active ingredient and a pharmaceutical carrier, comprising (I) at least one reagent for detecting the presence of (I) when bound to the RPTK, and instructions for use; (3) a method for treatment of bone and cartilage related disorders by administering a composition of (I) to the subject; (4) a method for treating or inhibiting a cell proliferative disease or disorder by administering the composition of (I); (S) a method for screening a molecule comprising the antigen-binding portion of an antibody which blocks ligand-dependent activation of RPTK; (6) an antibody which blocks ligand-dependent activation of RPTK; (6) an antibody which blocks ligand-dependent activation of RPTK; (6) and WH region; (8) vectors comprising a mucleic acid molecule of (6) or (7); and (9) host cells transformed with the vector: (I) have osteopathic, cycostatic and ophthalmological activities, and can be used as RPTK inhibitor. Compositions comprising (I) are useful for treating bone and cartilage disorders, including skeletal disorders such as skeletal dysplasia, severe achondroplasia, thanatophoric dysplasia, decondroplasia, decondroplasia, decondroplasia, decondroplasia, decondroplasia, decondroplasia, decondroplasia, decondroplasia, dec acanthosis nigricans dysplasia) or a craniosynostosis disorder (e.g. Muenke coronal craniosynostosis or Crouzon syndrome with acanthosis nigricans). The composition may also be used for treating or inhibiting

Example 2; Page 43; 122pp; English.

WPI; 2003-801317/75.

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malignant cell proliferative disease or disorder associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dependent FGFR signaling, such as vision disorders (e.g. neovascular glaucoma, macular degeneration and proliferative retinopathy including diabetic retinopathy, and non-neoplastic angiogenic pathologic conditions (e.g. haemanglomas, angiofibromas and psoriasis). The present sequence is given in the exemplification of the present invention.
                                       RETK activity, including a haematopoietic malignancy (e.g. multiple myeloma), solid tumours (e.g. mammary, colon, cervical, bladder, colorectal, chondrosarcoma or osteosarcoma), tumour formation, primary tumours, tumour progression (particularly progression of transitional cell carcinoma or mammary carcinoma), or tumour metastasis, where the cell proliferative disorder may be associated with the action of a constitutively activated RPTK, or with ligand-dependent activation of Myperproliferative diseases and disorders associated with ligand-
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Sequence 235 AA;

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64 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLAQDMLNGKEYKCKVSNKALPAPIEKT 123
                                                                                                                                                                                                                                                                                     180
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                                                                                                                                                                                                                                                                                                                     124 ISKAKGQPREPQVYTLPPSRDELTKNQVSLITCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                           4 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                           NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                       121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
                                                 ;
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97.2%; Score 1225; DB 6; Length 235; 97.0%; Pred. No. 1.6e-88; ive 3; Mismatches 4; Indels
                                                 Matches 225; Conservative
                           Similarity
                                                                                                                                                                                             61
       Query Match
                                Local
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Binding domain-immunoglobulin fusion protein-associated protein #101.
                                            ADD25647 standard; protein; 235 AA
                                                                                                                                      (first entry)
                                                                                                                                      15-JAN-2004
                                                                                         ADD25647;
SSULT 15
                        D25647
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Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidabetic; antithyroid; antiarthritic; immunosuppressive; antidabetic; antithyroid; characterive; hinge region; fusion heavy chain; CH2 constant region; IgG1, antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; andignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.

US2003118592-A1. Unidentified

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17-JAN-2001; 2001US-0367358P.
17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
                                                25-JUL-2002; 2002US-00207655
                                                                                                                                                                                                      (GENE-) GENECRAFT INC.
26-JUN-2003.
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Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;

PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSFGK

184

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The invention relates to a binding domain. Immunoglobulin heavy chain comprising a binding domain polypeptide that is fused to an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the CH2 constant region polypeptide. The immunoglobulin heavy chain CH3 constant region polypeptide that is fused to the CH2 constant region polypeptide. The immunoglobulin hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide comprises: where the mutated human IgG1 immunoglobulin hinge region polypeptide of polypeptide control of contains or cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (b) having 3 or more cysteine residues and a mutated human IgG1 immunoglobulin hinge region polypeptide contains or orysteine residues. The binding domain immunoglobulin hinge region polypeptide contains or orysteine residues. The binding domain immunoglobulin hinge region polypeptide contains or orysteine residues. The binding domain immunoglobulin hinge region polypeptide contains or orysteine residues. The binding domain immunoglobulin fusion protein, a host cell mediated cytotoxicity (ADCC) and complement fixation. The binding domain-immunoglobulin fusion protein, a recombinant expression construct comprising the binding domain-immunoglobulin fusion organizate, and treating a subject or subject dof having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for this patent formed mark of the printed sequence data for this patent formed mark of the printed sequence data for this patent formed mark of protein a malignant condit
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                                                             New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                segdata uspto gov/sequence.html?DooID=20030118592. The authors have not identified the sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.
                                                                                                                                                                                                                    invention relates to a binding domain-immunoglobulin fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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97.0%; Pred. No. 1.6e-88;
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                                                                                                                                                                 Disclosure; SEQ ID NO 208; 157pp; English
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Best Local Similarity
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Search completed: October 27, 2004, 16:59:37 Job time: 91.7544 secs

us-10-000-439-3.rag

Sequence 8, Appli Sequence 1, Appli Sequence 6, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 18, Appli Sequence 18, Appli Sequence 2, Appli Sequence 18, Appli

Sequence 20 Sequence 3 Sequence Sequence

Sequence

Sequence 8, Ag Sequence 72, 1 Sequence 5, Ag

Sequence 7, Sequence 7, Sequence 11, Sequence 9,

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61 NMYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT
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Best Local Similarity 100.0%; Pred. No. 9.8e-93;
Matches 232; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08847208
Publication No. US20030082190A1
GENERAL INFORMATION:
APPLICANT: Saxon, Andrew
APPLICANT: Zhang, Xe
APPLICANT: Zhang, Xe
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES;
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES;
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES;
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SEQ ID NO 3: SEQ ID NOS: 177
SEQ ID NO 3: Andrew
CONTRARE: FastSEQ for Windows Version 4.0
          US-10-452-646-9
US-10-157-408-7
US-10-097-044A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
US-09-847-208-3
                           LENGTH: 232
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121
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Sequence 2, Appli
Sequence 2, Appli
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Sequence 10, Appli
Sequence 10, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 28, Appli
Sequence 28, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 13, Appli
                                                                                               October 27, 2004, 17:04:05; Search time 71.0036 Seconds (without alignments) 1059.356 Million cell updates/sec
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1260
1 EPKSCDKTHICPPCPAPELL......MHEALHNHYQQRSLSLSPGK 232
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(gnz 6/ptodata//pubpaa/USO7 PUBCOMB.pep:*

(gnz 6/ptodata//pubpaa/USO7 NEW PUB.pep:*

(gnz 6/ptodata//pubpaa/USO6 NEW PUB.pep:*

(gnz 6/ptodata//pubpaa/USO6 NEW PUB.pep:*

(gnz 6/ptodata//pubpaa/USO7 NEW PUB.pep:*

(gnz 6/ptodata//pubpaa/USO8 PUBCOMB.pep:*

                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-617-619-7
US-10-761-593A-26
US-10-761-593A-26
US-10-76-555-208
US-09-996-357-13
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US-10-000-439-3

US-09-847-208-2

US-10-000-439-2

US-09-847-208-7

US-09-947-208-7

US-09-996-357-10
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Maximum Match 100%
Listing first 45 summaries
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CORGANISM: Homo sapiens
US-10-000-439-2
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                                 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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100.0%; Score 1260; DB 14; Length 232;
Best Local Similarity 100.0%; Pred. No. 9.8e-93;
Matches 232; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                         Sequence 3, Application US/10000439;
Sequence 3, Application US/10000439;
Publication No. US20030064063A1;
GENERAL INFORMATION:
TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR;
TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR;
TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES;
FILE REFERENCE: UC667.004A
CURRENT APPLICATION NUMBER: US/10/000,439;
CURRENT APPLICATION NUMBER: US 09/847,208
PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFFWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-3
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| Publication No. US20030082190A1
| GENERAL INFORMATION:
| APPLICANT: Saxon, Andrew
| APPLICANT: Shang, Ke
| APPLICANT: Zhu, Daocheng
| TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
| TITLE OF INVENTION:
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100.0%; Pred. No. 1.5e-92;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 232; Conservative
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US-10-000-439-2

Sequence 2, Application US/10000439

Publication No. US20330064063A1

GENERAL INFORMATION:
APPLICANT: Saxon, Andrew

TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES
FILE REFERENCE: UC067.004A

CURRENT APPLICATION NUMBER: US/10/000,439

CURRENT FILING DATE: 2001-0-24

PRIOR FILING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 330
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APPLICANT: Zhang, Ke
TITLE OF INVENTION: EVSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67,002A
CURRENT APPLICATION WUMBER: US/09/847,208
UNDMER OF SEQ ID NOS: 177
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Best Local Similarity 100.0%; Pred. No. 1.5e-92;
Matches 232; Conservative 0; Mismatches 0;
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; Publication No. US20030082190A1
; GENERAL INFORMATION:
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181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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LENGTH: 232
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                                                                                                                                        OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IgG1) to CH2-CH3-CH4 OTHER INFORMATION: (IgE) 09-847-208-7
                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                          DB 10; Length 569;
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/10000439
Publication No. US20030054063A1
GENERAL INFORMATION:
TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES
FILE REFERENCE: UCO67.004A
CURRENT APPLICATION NUMBER: US/10/000,439
CURRENT FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-05-01
                                                                                                                                                                                                                                        100.0%; Score 1260; DB 10;
100.0%; Pred. No. 2.8e-92;
vative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
IENCH: 569
TYPE: PRT
ORGANISM: Unknown
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7 LENGTH: 569
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Best Local Similarity 100.
Matches 232; Conservative
                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 232; Conservative
                           LENGTH: 569
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER
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APPLICANT: Isreal, David I
APPLICANT: Isreal, David I
APPLICANT: Isreal, David I
APPLICANT: Gosselin, Michael
APPLICANT: Gosselin, Michael
TITLE OF INVENTION: THERABEUTIC AGENTS AND METHODS OF USE THEREOF FOR
TITLE OF INVENTION: THERABEUTIC AGENTS AND METHODS OF USE THEREOF FOR
TITLE OF INVENTION: THERABEUTIC ASSOCIATION OF THE REPRESSENCE: PRICKET ON WIMBER: US/09/996,357
CURRENT FILING DATE: 2001-11-27
PRICK APPLICATION NUMBER: 60/253,302
PRICK APPLICATION NUMBER: 60/253,108
PRICK APPLICATION NUMBER: 60/250,198
PRICK APPLICATION NUMBER: 60/250,198
PRICK APPLICATION NUMBER: 60/250,198
PRICK APPLICATION NUMBER: 60/250,198
PRICK PILING DATE: 2000-11-29
PRICK PILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PARENTIN VEF: 2.0
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APPLICANT: Wooden, Michael B.
APPLICANT: Mann, Michael B.
APPLICANT: Dunstan, Colin R.
TITLE OF INVENTION: DOG Fusion Protein Compositions and Methods FILE REPERENCE: A-604
CURRENT APPLICATION NUMBER: US/09/389,782
CURRENT FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 6.1e-90;
3; Mismatches 4;
US-09-996-357-10
; Sequence IO, Application US/09996357
; Patent No. US20020133001A1
; GENERAL INPORMATION:
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Publication No. US20030144187A1
GENERAL INFORMATION:
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Best Local Similarity 97.0%;
Matches 225; Conservative 3
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Gaps

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TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological TITLE OF INVENTION: activities FILE REPERNOG: 0.2SUN2001-A CURRENT APPLICATION NUMBER: US/10/761,593A CURRENT APPLICATION NUMBER: 0.004-01-21 PRIOR APPLICATION NUMBER: 0.09/932812 PRIOR APPLICATION NUMBER: 0.09/932812 PRIOR FILING DATE: 2001-08-17 NUMBER OF SEQ ID NOS: 28 SOFTWARE: Patentin version 3.2 SEQ ID NO 505 20 PRIOR PRI
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CURRENT APPLICATION NUMBER: US/10/207,655
NUMBER OF SEQ ID NOS: 4266
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 97.2%; Score 1225; DB 16; Length 232; Best Local Similarity 97.0%; Pred. No. 6.1e-90; Matches 225; Conservative 3; Mismatches 4; Indels 0
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ORGANISM: Homo sapiens
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US-10-207-655-208
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Publication No. US20040110929A1
GENERAL INFORMATION:
APPLICANT: Blorn, Soren E
APPLICANT: Blorn, Soren E
APPLICANT: Micolaisen, Else M
APPLICANT: Micolaisen, Anker S
TITLE OF INVENTION: TP Binding Compound
FILE REFERENCE: 6455_200-US
CURRENT APPLICATION NUMBER: US/10/617,619
CURRENT FILING DATE: 2003-07-11
PRIOR PLICATION NUMBER: US 60/404,568
PRIOR FILING DATE: 2002-07-12
PRIOR PLICATION NUMBER: US 60/404,568
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Version 3.2
SOFTWARE: Patentin Version 3.2
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Pred. No. 6.1e-90;
3; Mismatches 4;
                     Pred. No. 6.1e-90; 3; Mismatches 4
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US-10-761-593A-26
; Sequence 26, Application US/10761593A
; Publication No. US20040175824A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Cecily R
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                 97.0%;
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Best Local Similarity 97.0
Matches 225; Conservative
                 Best Local Similarity 97.0
Matches 225; Conservative
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US-10-617-619-7
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Sequence 12, Application US/0996357
Patent No. US20020133001A1
GENERAL INFORMATION:
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Best Local Similarity 97.04
Matches 225; Conservative
                                                            Best Local Similarity 97.0
Matches 225; Conservative
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ORGANISM: Homo Sapiens
US-10-152-363A-6
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US-10-008-063-18
                                       Query Match
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APPLICANT: Geter, Malcolm L
APPLICANT: Setel, David I
APPLICANT: Secal, David I
APPLICANT: Secal, David I
APPLICANT: Goselin, Michael
APPLICANT: Goselin, Michael
TITLE OF INVENTION: TREATING AN AMYLOIDOGENIC DISEASE
TITLE OF INVENTION: TREATING AN AMYLOIDOGENIC DISEASE
FILE REFERENCE: PPI-105
CURRENT FILING DATE: 2001-11-27
PRIOR PLILING DATE: 2001-11-27
PRIOR PAPLICATION NUMBER: 60/253,302
PRIOR PAPLICATION NUMBER: 60/250,198
PRIOR PLILING DATE: 2000-11-29
PRIOR PLILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PALENTIN Ver: 2.0
SEQ ID NO 13
LENGTH: 247
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                       184 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 235
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APPLICANT: Xu, Wenfeng
APPLICANT: Henne, Randal M.
APPLICANT: Henne, Randal M.
APPLICANT: Henne, Randal M.
APPLICANT: Henne, Randal M.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
FILE REFERENCE: 00-103
CURRENT APPLICATION UNBER: US/10/008,063
CURRENT PILING DATE: 2001-11-05
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 251
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97.0%; Pred. No. 6.6e-90;
iive 3; Mismatches 4;
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Sequence 18, Application US/10008063
Bequence 18, Application US/10008063
Bublication No. US20030092164A1
GENERAL INFORMATION:
APPLICANT: Gross, Jane A.
                                                                                                                                               Sequence 13, Application US/09996357
Patent No. US20020133001A1
GENERAL INFORMATION:
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Best Local Similarity 97.0
Matches 225; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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181
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                                                                                                                                                                                                                                                                                                                                                                                                                                       140 ISKAKGOPREPOVYTLPPSRDELTKNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTTP 199
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                                                                                                                                                                    20 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                               1 BPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSFGK 251
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Score 1225; DB 14; Length 251; Pred. No. 6.7e-90; 3; Mismatches 4; Indels 0
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Pred. No. 6.7e-90;
3; Mismatches 4; Indels 0
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APPLICANT: Isreal, David I
APPLICANT: Joyal, John L
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### APPLICANT: Gosselin, Michael
### TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR
### TITLE OF INVENTION: TREATING AN AMYLOIDOGENIC DISEASE
### TITLE OF INVENTION: TREATING AND AMYLOIDOGENIC DISEASE
### CURRENT APPLICATION NUMBER: US/09/996,357
### CURRENT FILING DATE: 2001-11-27
### PRIOR APPLICATION NUMBER: 60/253,302
### PRIOR FILING DATE: 2000-11-29
### PRIOR FILING DATE: 2000-11-29
### PRIOR APPLICATION NUMBER: 60/250,186
### PRIOR APPLICATION NUMBER: 60/257,186
### PRIOR PRIOR OF SEQ ID NOS: 13
### SOFTWARE: Patentin Ver. 2.0
### CHANTISM: Artificial Sequence
### COMPANISM: Artificial Sequence
### COTHER INFORMATION: Description of Artificial Sequence: alpha-beta(16-30)FC
US-09-996-357-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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97.2%; Score 1225; DB 9;
Best Local Similarity 97.0%; Pred. No. 7.2e-90;
Matches 225; Conservative 3; Mismatches 4;
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Search completed: October 27, 2004, 17:20:19 Job time : 72.0036 secs